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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Mon Mar 8 23:35:29 1999; MasPar time 72.58 Seconds  
879.119 Million cell updates/sec  
Tabular output not generated.  
Title: >US-09-206-040-1  
Description: (1489) from US09206040A.seq  
Perfect Score: 465  
N.A. Sequence: 1 ttaactgtcagcgcgcaggt.....gatgatacattgaagatnnt 469  
Comp: aattgaacgtgcgcnggtcca.....ctactatgtaacttcanna

Scoring table: TABLE jmetric  
Gap 60  
Nmatch STD : Dbase 0; Query 0  
Searched: 188442 seqs, 68026449 bases x 2  
Post-processing: Minimum Match 08  
Listing first 45 summaries

Database: n-geneseq32  
1:part2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
24:part24 25:part25 26:part26 27:part27 28:part28  
29:part29 30:part30 31:part31 32:part32 33:part33  
34:part34 35:part35 36:part36 37:part37 38:part38  
39:part39 40:part40

Statistics: Mean 7.077; Variance 2.661; scale 2.659  
Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES						
Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	28	6.0	570	T91275	cdna encoding a novel	1.36e-09
2	28	6.0	969	T96721	Human synaptogyrin cd	1.36e-09
3	28	6.0	1581	T32233	Cuphea C14-0-ACP thio	1.36e-09
4	28	6.0	1898	40	Human MKK3-interactin	1.36e-09
5	21	4.5	1257	24	54 gene differentia	1.09e-03
6	21	4.5	2055	24	10 gene differentia	1.09e-03
7	18	3.9	36	13	Primer SALADrt contg.	2.20e-01
8	18	3.9	787	21	Parietaria allergen p	2.20e-01
9	18	3.9	845	21	Parietaria allergen p	2.20e-01
10	18	3.9	1930	40	CDNA encoding human C	2.20e-01
11	18	3.9	1930	18	CROC-1 cdna encodes c	2.20e-01
12	18	3.9	2721	2	BamHI J-I fragment ca	2.20e-01
13	18	3.9	2721	2	BamHI J-I fragment ca	2.20e-01

14	17	3.7	26	36	T98445	Template switching ol	1.17e+00
15	17	3.7	35	13	Q79346	Primer SALAD for the	1.17e+00
16	17	3.7	543	35	T39800	Human clone 34 gene	1.17e+00
17	17	3.7	925	40	V16740	CDNA encoding human C	1.17e+00
18	17	3.7	925	18	T15611	CROC-4 cdna encodes c	1.17e+00
19	17	3.7	946	13	Q80219	Human NDF-alpha3 clon	1.17e+00
20	17	3.7	1003	35	T85935	Rat epithelial membra	1.17e+00
21	17	3.7	1098	13	Q80225	Rat NDF clone 4 DNA.	1.17e+00
22	17	3.7	1101	34	T74988	Interferon gamma indu	1.17e+00
23	17	3.7	1101	34	T74987	Interferon gamma indu	1.17e+00
24	17	3.7	1261	13	Q80230	Rat NDF clone 40 DNA.	1.17e+00
25	17	3.7	1651	13	Q80218	Human NDF-alpha2b clo	1.17e+00
26	17	3.7	1865	40	T9584	Bovine platelet activ	1.17e+00
27	17	3.7	1700	16	Q96100	Sequence encoding hum	1.17e+00
28	17	3.7	1734	35	T39792	Human SH3P9 gene.	1.17e+00
29	17	3.7	1784	38	T93211	Mouse neurotactin CDN	1.17e+00
30	17	3.7	1807	13	Q80217	Human NDF-alpha2b clo	1.17e+00
31	17	3.7	1983	26	T47497	Porcine growth hormon	1.17e+00
32	17	3.7	2232	37	T95700	Novel human gene, des	1.17e+00
33	17	3.7	2288	32	T72894	Plasmodium ebl-1 gene	1.17e+00
34	17	3.7	2288	14	Q83526	P. falciparum EBL-el	1.17e+00
35	17	3.7	2531	13	Q80227	Rat NDF clone 20 DNA.	1.17e+00
36	17	3.7	2606	14	Q83527	P. falciparum E3la ge	1.17e+00
37	17	3.7	2806	32	T72895	Plasmodium E3la gene.	1.17e+00
38	17	3.7	2712	24	T38265	200 gene differential	1.17e+00
39	17	3.7	2743	13	Q80231	Rat NDF clone 41 DNA.	1.17e+00
40	17	3.7	2914	13	Q80226	Rat NDF clone 19 DNA.	1.17e+00
41	17	3.7	3097	31	T69590	Murine short form Ob	1.17e+00
42	17	3.7	3451	38	V02308	Cell membrane proton-	1.17e+00
43	17	3.7	3854	31	T69591	Murine long form Ob r	1.17e+00
44	17	3.7	5030	36	T75702	pGreenlntern vector.	1.17e+00
45	16	3.4	925	40	V16740	CDNA encoding human C	5.89e+00

ALIGNMENTS

RESULT 1  
ID T91275 standard; cdna; 570 BP.  
AC T91275;  
DT 23-APR-1998 (first entry)  
DE CDNA encoding a novel beta-chemokine designated PTEC.  
KW Beta-chemokine; PTEC; homologue; human RANTES; C-C chemokine;  
KW diagnosis; treatment; activated T cell;  
KW immediate type hypersensitivity; leukocyte proliferation; ss.  
FH Homo sapiens.  
FT Key Location/Qualifiers  
CDS 110..391 /\*tag= a  
PN WO9739126-A1.  
PD 23-OCT-1997.  
PF 14-APR-1997; U06249.  
PR 17-APR-1996; US-633682.  
PA (INCY-) INCYTE PHARM INC.  
PI Bandman O, Hawkins PR, Murry LE;  
DR WPI; 97-526462/48.  
P-PSDB; W27271.  
PT PTEC, a novel human beta-chemokine - useful for diagnosing and  
PT treating e.g. viral, bacterial, fungal infections, auto-immune  
PT diseases, etc  
PS Claim 2; pages 39-40; 59pp; English.  
CC The present DNA sequence encodes a novel beta-chemokine polypeptide  
CC designated PTEC. The protein has Cys residues of a beta-chemokine (C32,  
CC C33, C56 and C72). The present sequence was isolated from a cDNA library  
CC generated from non-tumorous human prostate tissue. The PTEC protein is  
CC a homologue of human RANTES, which is a C-C chemokine with structural  
CC similarity to interleukin-8 and human MIP-beta. The polynucleotide  
CC sequence encoding PTEC can be used to diagnose or treat a condition  
CC associated with the presence of activated T cells including viral,  
CC bacterial, fungal or helminthic infections, allergic or asthmatic  
CC responses, mechanical injury associated with trauma, arteriosclerosis,  
CC atherogenesis or collagen vascular diseases, autoimmune diseases such as  
CC rheumatoid arthritis, myasthenia gravis, systemic lupus erythematosus or  
CC haemolytic anaemia, leukaemia, lymphomas or carcinomas, and diseases of

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FT cds 119..1354
FT /*tag= a
FT
FT WO9623892-A2.
FT 08-AUG-1996.
FT PF 01-FEB-1996; U01585.
FT PR 02-FEB-1995; US-383756.
FT PA 05-JUN-1995; US-460898.
FT (CALJ ) CALGENE INC.
FT Dehesh K, Hawkins D, Voelker TA;
FT WPI: 96-371439/37.
FT P-PSDB; W02081.
FT Recombinant prodn. of myristate in plant cells - using DNA with
FT preferential activity on C14 fatty acids from Cuphea palustris,
FT nutmeg and camphor, useful in detergent and food industries
FT Example 1; Fig 1A-1E; 77pp; English.
FT PS
FT A cDNA clone (T32233), designated MCT314 (pCpFatB2), codes for Cuphea
FT palustris C14:0-ACP thioesterase (W02081), an enzyme that acts
FT primarily on C14:0-ACP substrates, forming C14:0 (myristate). It
FT was isolated from a developing seed cDNA library by screening with
FT sequences encoding medium-chain acyl-ACP thioesterases from Cuphea
FT hookeriana. Constructs for expression of clone MCT34 in plant seeds
FT under the control of napin or oleosin regulatory regions were prepd.
FT These allow high-level prodn. of myristate (useful in surfactants
FT and foods) in plant cells, e.g. Brassica.
FT SQ Sequence 1581 BP; 418 A; 356 C; 410 G; 397 T;
FT
FT Query Match 6.0%; Score 28; DB 22; Length 1581;
FT Best Local Similarity 100.0%; Pred. No. 1.36e+09;
FT Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT
FT Db 54 ggaattcccggtcgaccacgcgtccg 81
FT |||||||
FT QY 29 ggaattcccggtcgaccacgcgtccg 56
FT
FT RESULT 4
FT ID V17199 standard; cDNA; 1698 BP.
FT AC V17199;
FT DT 10-JUN-1998 (first entry)
FT DE Human MKK3-interacting protein (MIP) encoding cDNA.
FT KW MKK3-interacting protein; MIP; mitogen activated protein kinase;
FT KW MAPK kinase-3; human; transduction; target; extracellular signal;
FT KW interfering mutant; ss.
FT OS Homo sapiens.
FT FH Key Location/Qualifiers
FT FT CDS 167..1213
FT /*tag= a
FT /product= "MKK3-interacting protein"
FT
FT WO9800539-A2.
FT 08-JAN-1998.
FT PF 02-JUL-1997; U10866.
FT PR 01-JUL-1997; US-886572.
FT PA 03-JUL-1996; US-021224.
FT (CHIR ) CHIRON CORP.
FT Kavanaugh MW, Shvamaia V;
FT WPI: 98-086965/08.
FT P-PSDB; W52169.
FT Human MKK3-interacting protein, used to identify human tissues in
FT malignant conditions - comprises nucleic acid, antibodies, fusion
FT proteins and peptide fragments
FT Disclosure; Page 14; 17pp; English.
FT PS
FT This cDNA encodes a human MKK3-interacting protein (MIP). The mitogen-
FT activated protein kinase (MAPK) kinase-3 (MKK3) is a protein kinase that
FT phosphorylates p38 MAP kinase specifically and is involved in transducing
FT stress signals. The MIP binds to and interacts with a dominant
FT interfering mutant form of MKK3 and may be involved in transducing
FT extracellular signals to the nucleus, resulting in activation of p38
FT kinase. MIP is expressed in human brain, kidney, liver, lung, pancreas
FT and spleen but not in heart or striated muscle. Detection of MIP in a
FT body sample (particularly a tumour or metastasis) is used to identify the
FT tissue source, the tissue selected from the group consisting of brain,
FT kidney, liver, lung, pancreas or spleen tissue. Fusion proteins comprising

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CC at least 8 contiguous amino acids of MIP fused to a second protein  
 CC sequence can be used to target MIP, or its peptides, to specific cells or  
 CC tissues. They can be used as a source of MIP in assays and also as  
 CC immunogen. The MIP encoding nucleic acid is used for expression of  
 CC recombinant MIP polypeptides and as a source of probes for detecting  
 CC MIP-related mRNA.  
 SQ Sequence 1698 BP; 455 A; 381 C; 449 G; 413 T;

Query Match 6.0%; Score 28; DB 40; Length 1698;  
 Best Local Similarity 100.0%; Pred. No. 1.36e-09;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 75 ggaattccgggtcgaccacgcgtccg 102  
 |||||  
 QY 29 ggaattccgggtcgaccacgcgtccg 56

## RESULT 5

ID T38266 standard; cDNA; 1257 BP.

AC T38266;

DT 29-DEC-1996 (first entry)

DE 54 gene differentially expressed in T helper cells.

KW T helper cell; TH cell; T-cell; T-lymphocyte; 54 gene;

KW differential expression; immune disorder; multiple sclerosis;

KW asthma; lepromatous leprosy; diagnosis; therapy;

KW cysteine protease; ss.

OS Mus sp.

FS Key

FT cds

FT mat\_peptide

FT misc\_difference 1147

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AC T38260;  
 DT 29-DEC-1996 (first entry)  
 DE 10 gene differentially expressed in T helper cells.  
 KW T helper cell; TH cell; T-cell; T-lymphocyte; 10 gene;  
 KW differential expression; immune disorder; multiple sclerosis;  
 KW asthma; lepromatous leprosy; diagnosis; therapy; ss.  
 OS Mus sp.  
 FS Key

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 CC tissues. They can be used as a source of MIP in assays and also as  
 CC immunogen. The MIP encoding nucleic acid is used for expression of  
 CC recombinant MIP polypeptides and as a source of probes for detecting  
 CC MIP-related mRNA.  
 SQ Sequence 1698 BP; 455 A; 381 C; 449 G; 413 T;

Query Match 6.0%; Score 28; DB 40; Length 1698;  
 Best Local Similarity 100.0%; Pred. No. 1.36e-09;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 75 ggaattccgggtcgaccacgcgtccg 102  
 |||||  
 QY 29 ggaattccgggtcgaccacgcgtccg 56

## RESULT 5

ID T38266 standard; cDNA; 1257 BP.

AC T38266;

DT 29-DEC-1996 (first entry)

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KW T helper cell; TH cell; T-cell; T-lymphocyte; 54 gene;

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FS Key

FT cds

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CC at least 8 contiguous amino acids of MIP fused to a second protein  
 CC sequence can be used to target MIP, or its peptides, to specific cells or  
 CC tissues. They can be used as a source of MIP in assays and also as  
 CC immunogen. The MIP encoding nucleic acid is used for expression of  
 CC recombinant MIP polypeptides and as a source of probes for detecting  
 CC MIP-related mRNA.  
 SQ Sequence 1698 BP; 455 A; 381 C; 449 G; 413 T;

Query Match 6.0%; Score 28; DB 40; Length 1698;  
 Best Local Similarity 100.0%; Pred. No. 1.36e-09;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 75 ggaattccgggtcgaccacgcgtccg 102  
 |||||  
 QY 29 ggaattccgggtcgaccacgcgtccg 56

## RESULT 5

ID T38266 standard; cDNA; 1257 BP.

AC T38266;

DT 29-DEC-1996 (first entry)

DE 54 gene differentially expressed in T helper cells.

KW T helper cell; TH cell; T-cell; T-lymphocyte; 54 gene;

KW differential expression; immune disorder; multiple sclerosis;

KW asthma; lepromatous leprosy; diagnosis; therapy;

KW cysteine protease; ss.

OS Mus sp.

FS Key

FT cds

FT mat\_peptide

FT misc\_difference 1147

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CC at least 8 contiguous amino acids of MIP fused to a second protein  
 CC sequence can be used to target MIP, or its peptides, to specific cells or  
 CC tissues. They can be used as a source of MIP in assays and also as  
 CC immunogen. The MIP encoding nucleic acid is used for expression of  
 CC recombinant MIP polypeptides and as a source of probes for detecting  
 CC MIP-related mRNA.  
 SQ Sequence 1698 BP; 455 A; 381 C; 449 G; 413 T;

Query Match 6.0%; Score 28; DB 40; Length 1698;  
 Best Local Similarity 100.0%; Pred. No. 1.36e-09;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 75 ggaattccgggtcgaccacgcgtccg 102  
 |||||  
 QY 29 ggaattccgggtcgaccacgcgtccg 56

## RESULT 5

ID T38266 standard; cDNA; 1257 BP.

AC T38266;

DT 29-DEC-1996 (first entry)

DE 54 gene differentially expressed in T helper cells.

KW T helper cell; TH cell; T-cell; T-lymphocyte; 54 gene;

KW differential expression; immune disorder; multiple sclerosis;

KW asthma; lepromatous leprosy; diagnosis; therapy;

KW cysteine protease; ss.

OS Mus sp.

FS Key

FT cds

FT mat\_peptide

FT misc\_difference 1147

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CC nucleotides 7-1826 and 726-3225 of Q79326. In this sequence, about  
 CC 1200 nts preceded the ARE region without a stop codon in the same  
 CC ORF. To further characterise the 5' terminus of this cDNA, 5'-RACE  
 CC was carried out with the poly A+ RNA from IMR-32 human  
 CC neuroblastoma cells. The poly A+ RNA was reverse transcribed with  
 CC primer JK721RC. The products were tailed and subcloned to PCR with  
 CC primers SALAD and SALADT and JK723RII. TE was added to the PCR  
 CC products and a second PCR amplification was carried out using  
 CC primers SALAD and JKNOT. Following transfection of the reverse  
 CC transcribed, PCR amplified sequences into competent DH5-alpha  
 CC cells, clones corresp. to ARD 1 were isolated.  
 SQ Sequence 36 BP: 4 A; 12 C; 11 G; 9 T;

Query Match 3.9%; Score 18; DB 13; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.20e-01;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 ggtcgaccacgcgtccg 36  
 |||||

Qy 40 gtcgaccacgcgtccg 57

# RESULT 8

ID T29008 standard; cDNA; 787 BP.

AC T29008;

DT 16-SEP-1996 (first entry)

DE Parietaria allergen PJ003 PAR70 cDNA (preliminary sequence).

KW Allergen; pollen; pollinosis; desensitisation; immunotherapy;

KV vaccine; hayfever; ds.

OS Parietaria judaica.

PN EP-707065-A2.

PD 17-APR-1996.

PF 24-JUL-1995; 401754.

PR 22-JUL-1994; US-279113.

PA (UYMA-) UNIV MANITOBA.

PI Mohapatra SS;

PT WPI; 96-201752/21.

PT DNA encoding Parietaria sp. pollen allergen - useful in

PT immuno-therapy and desensitisation of allergies

PS Claim 4; Fig 3f; 34pp; English.

CC Screening of a Parietaria pollen library with antisera to a 14 kDa

CC pollen protein from Parietaria led to the identification of 3 groups

CC of cDNA clones encoding allergenic proteins: group I (PJ001)

CC comprises clones PAR64, PAR16, PAR5, PAR21, PAR48, PAR39 and

CC PAR9 (T29000-06) encoding 7 isoallergens (R97300-06); group II (PJ009)

CC comprises clone PAR19 (T29007) encoding 2 isoallergens (R97307-08);

CC and group III (PJ003) comprising clones PAR70 and PAR10 (T29008-09;

CC preliminary sequence data) with 3 isoallergenic variants. The cDNA

CC clones can be used as probes to identify other allergen sequences, or

CC for prodn. of recombinant allergens useful in the diagnosis and

CC immunotherapy of allergic diseases induced by Parietaria.

SQ Sequence 787 BP; 239 A; 189 C; 167 G; 192 T;

Query Match 3.9%; Score 18; DB 21; Length 787;

Best Local Similarity 100.0%; Pred. No. 2.20e-01;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 11 ggtcgaccacgcgtccg 28  
 |||||

Qy 39 ggtcgaccacgcgtccg 56

# RESULT 9

ID T29009 standard; cDNA; 845 BP.

AC T29009;

DT 16-SEP-1996 (first entry)

DE Parietaria allergen PJ003 PAR10 cDNA (preliminary sequence).

KW Allergen; pollen; pollinosis; desensitisation; immunotherapy;

KV vaccine; hayfever; ds.

OS Parietaria judaica.

PN EP-707065-A2.

PD 17-APR-1996.

PF 24-JUL-1995; 401754.

PR 22-JUL-1994; US-279113.

PA (UYMA-) UNIV MANITOBA.

PI Mohapatra SS;

DR WPI; 96-201752/21.

PT DNA encoding Parietaria sp. pollen allergen - useful in

PT immuno-therapy and desensitisation of allergies

PS Claim 4; Fig 3f; 34pp; English.

CC Screening of a Parietaria pollen library with antisera to a 14 kDa

CC pollen protein from Parietaria led to the identification of 3 groups

CC of cDNA clones encoding allergenic proteins: group I (PJ001)

CC comprises clones PAR64, PAR16, PAR5, PAR21, PAR48, PAR39 and

CC PAR9 (T29000-06) encoding 7 isoallergens (R97300-06); group II (PJ009)

CC comprises clone PAR19 (T29007) encoding 2 isoallergens (R97307-08);

CC and group III (PJ003) comprising clones PAR70 and PAR10 (T29008-09;

CC preliminary sequence data) with 3 isoallergenic variants. The cDNA

CC clones can be used as probes to identify other allergen sequences, or

CC for prodn. of recombinant allergens useful in the diagnosis and

CC immunotherapy of allergic diseases induced by Parietaria.

SQ Sequence 845 BP; 260 A; 194 C; 183 G; 208 T;

Query Match 3.9%; Score 18; DB 21; Length 845;

Best Local Similarity 100.0%; Pred. No. 2.20e-01;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 5 ggtcgaccacgcgtccg 22  
 |||||

Qy 39 ggtcgaccacgcgtccg 56

# RESULT 10

ID V16738 standard; cDNA; 1930 BP.

AC V16738;

DT 18-JUN-1998 (first entry)

DE cDNA encoding human CROC-1 protein.

KW CROC-1; activating protein; promoter; proto-oncogene; c-fos;

KV antagonist; ds.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..516

FT /\*tag= a

FT /product= CROC-1

FT US5736331-A.

PN 07-APR-1998.

PD 18-OCT-1995; 544900.

PF 08-JUL-1994; US-272412.

PR (SCHE ) SCHERING CORP.

PA Lin SL, Rothofsky ML;

PI WPI; 98-239204/21.

DR P-PSDB; W46892.

PT c-fos Promoter-activating proteins - assay for nucleic acids

PT encoding such proteins, assay for antagonists, etc.

PS Claim 16; Columns 15-18; 12pp; English.

CC The present sequence encodes a novel human protein, designated CROC-1.

CC The protein is an activating protein of promoter of the proto-oncogene

CC c-fos. The specification describes a mammalian cell line whose cells

CC contain a recombinant expression vector comprising a reporter operatively

CC linked to a human c-fos promoter and a second expression vector

CC comprising a nucleic acid encoding that activates the human c-fos

CC promoter (e.g. CROC-1). Antigenic fragments of the CROC-1 protein can be

CC used to prepare antibodies, which are used to assay for or purify the

CC activating protein. Antagonists of the CROC-1 protein bind to, but do not

CC activate, the human c-fos promoter.

SQ Sequence 1930 BP; 524 A; 487 C; 404 G; 515 T;

Query Match 3.9%; Score 18; DB 40; Length 1930;

Best Local Similarity 100.0%; Pred. No. 2.20e-01;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 ggtcgaccacgcgtccg 72  
 |||||

Qy 39 ggtcgaccacgcgtccg 56

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RESULT 11
ID T15610 standard; cDNA; 1930 BP.
AC T15610;
DE 25-JUN-1996 (first entry)
DE CROC-1 cDNA encodes c-fos promoter activating protein.
KW CROC-1; CROC-4; c-fos promoter activating protein; signal transducer;
KW polyomavirus large T antigen; db.
OS Homo sapiens.
FH Key Location/Qualifiers
FT 1..516
FT /*tag= a
FT /product= CROC-1
FT
PN W09601899-A1.
PD 25-JAN-1996.
PF 05-JUL-1995; U07874.
PR 08-JUL-1994; US-272412.
PA (SCHE ) SCHERING CORP.
PI Lin SL, Rothofsky ML.
DR WPI; 96-097629/10.
DR P-PSDB; R90769.
PT Mammalian cell lines contg. recombinant vectors encoding c-fos
PT promoter activating proteins - used to identify nucleic acids
PT encoding signal transducing molecules which activate promoters.
PS Claim 13; Page 29-31; 41pp; English.
CC CROC-1 cDNA encodes a c-fos promoter activating protein of approx. 19 kD
CC with an acidic amino terminal half and a basic carboxy terminus. The
CC protein includes a kinase target domain which contains phosphorylation
CC sites for a variety of kinases involved in signal transduction. CROC-1
CC mRNA is approx. 2.3 kb in length and present in all tissues examined.
CC The cDNA is used in vectors, operatively linked to a nucleic acid
CC encoding a polyomavirus large T antigen. Mammalian cell lines contg.
CC these vectors, and vectors comprising a polyoma origin of replication
CC and a nucleic acid suspected to encode and activating protein of the
CC promoter, can be used to identify signal transducing molecules.
SQ Sequence 1930 BP; 524 A; 487 C; 404 G; 515 T;

Query Match 3.9%; Score 18; DB 18; Length 1930;
Best Local Similarity 100.0%; Pred. No. 2.20e-01;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 ggtagcaccacgcgctccg 72
QY 39 ggtagcaccacgcgctccg 56
|||||

RESULT 12
ID Q10543 standard; DNA; 2721 BP.
AC Q10543;
DE 27-MAR-1991 (first entry)
DE BamHI J-I fragment carrying sequences characteristic of latent
DE pseudorabies virus.
KW PRV; SS.
OS Pseudorabies virus.
PN US7537855-A.
PD 18-DEC-1990.
PF 13-JUN-1990; 238940.
PR 13-JUN-1990; US-537855.
PA (USDA ) US AGRIC RES SERV.
PI Cheung AK;
DR WPI; 91-021957/03.
PT Pseudo-raabies nucleotide sequences - used for producing
PT nucleic acid probes, antigens and antibodies for distinguishing
PT latent from productive infection
PS Disclosure; Page 22; 27pp; English.
CC The fragment carries sequences characteristic of the latent
CC pseudorabies viral genome, and may be used as a probe in diagnosis
CC of infection.
SQ Sequence 2721 BP; 428 A; 1007 C; 1017 G; 269 T;

Query Match 3.9%; Score 18; DB 2; Length 2721;
Best Local Similarity 100.0%; Pred. No. 2.20e-01;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 ggtagcaccacgcgctccg 72
QY 39 ggtagcaccacgcgctccg 56
|||||

RESULT 13
ID Q10212 standard; DNA; 2721 BP.
AC Q10212;
DE 27-MAR-1991 (first entry)
DE BamHI J-I fragment carrying sequences characteristic of productive
DE pseudorabies virus.
KW PRV; SS.
OS Pseudorabies virus.
PN US7537855-A.
PD 18-DEC-1990.
PF 13-JUN-1990; 238940.
PR 13-JUN-1990; US-537855.
PA (USDA ) US AGRIC RES SERV.
PI Cheung AK;
DR WPI; 91-021957/03.
PT Pseudo-raabies virus nucleotide sequences - used for producing
PT nucleic acid probes, antigens and antibodies for distinguishing
PT latent from productive infection
PS Disclosure; Page 21; 27pp; English.
CC The fragment carries sequences characteristic of the productive
CC pseudorabies viral genome, and may be used as a probe in diagnosis
CC of infection.
SQ Sequence 2721 BP; 428 A; 1007 C; 1017 G; 269 T;

Query Match 3.9%; Score 18; DB 2; Length 2721;
Best Local Similarity 100.0%; Pred. No. 2.20e-01;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 141 ctctctttccccccccc 158
Cp 96 ctctctttccccccccc 79
|||||

RESULT 14
ID T98445 standard; DNA; 26 BP.
AC T98445;
DE 11-MAR-1998 (first entry)
DE Template switching oligonucleotide Na21-G5p.
KW Template switching oligonucleotide; RNA/DNA hybrid; DNA preparation;
KW cDNA synthesis primer; cDNA cloning; cDNA library construction; SS.
OS Synthetic.
FH Key Location/Qualifiers
FT misc_RNA 22..26
FT /*tag= a
FT modified_base 26
FT /*tag= b
FT /*note= "phosphorylated"
FT
PN W09724455-A2.
PD 10-JUL-1997.
PF 03-JAN-1997; U00368.
PR 03-JAN-1996; US-582562.
PA (CLON-) CLONTECH LAB INC.
PI Chenchak A, Diatchenko L, Siebert P, Zhu Y;
DR WPI; 97-363690/33.
PT Preparation of cDNA from RNA molecules - by annealing cDNA synthesis
PT primer to RNA, synthesising DNA and contacting with novel template
PT switching oligo;nucleotide
PS Claim 9; Page 29; 39pp; English.
CC T98426-T98496 represent template switching oligonucleotides (TSO) used in
CC the method of the invention. The method of the invention is for preparing
CC DNA complementary to the 5'-end of an RNA molecule. The method comprises
CC annealing a cDNA synthesis primer (such as T98497) to the RNA molecule
CC and synthesising a first DNA strand complementary to at least a portion
CC of the RNA molecule, and contacting the RNA molecule with a TSO having a
CC pre-selected nucleotide sequence at its 5'-end and at least 1 riboguanine
CC residue at its 3'-end, where the TSO binds the 5'-end of the RNA molecule
CC and serves as a template for the extension of the 3'-end of the first DNA
CC strand. The method can be used for the synthesis and cloning of full

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CC length cDNA, or fragments, that correspond to the complete sequence of  
CC the 5'-end of the mRNA molecule. It can be used to construct cDNA  
CC libraries from nanogram quantities of total or poly A+ RNA. The TSO  
CC allows for negative selection against cDNA that are not complementary to  
CC the 5'-end of the template RNA, while allowing full length cDNA to be  
CC readily selected.  
SQ Sequence 26 BP; 8 A; 3 C; 12 G; 3 T;

Query Match 3.7%; Score 17; DB 36; Length 26;  
Best Local Similarity 100.0%; Pred. No. 1.17e+00;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 aagacgacagaaggagg 26  
|||||  
Qy 68 aagacgacagaaggagg 84

## RESULT 15

ID Q79346 standard; cDNA; 35 BP.  
AC Q79346;  
DT 05-JUN-1995 (first entry)  
DE Primer SALAD for the analysis of ARD 1.  
KW ADP-ribosylation factor; ARF; ARD 1; Primer; ss.  
OS Synthetic.  
PN WO9424283-A.  
PD 27-OCT-1994.  
PF 15-APR-1994; U04190.  
PR 16-APR-1993; US-049252.  
PR 19-APR-1993; US-049473.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
PI Mishima K, Moss J, Nightingale M, Tsuchiya M;  
DR WPI; 94-341862/42.  
PT GTP-binding protein ARD1 with ADP-ribosylation factor domain -  
PT useful as biochemical and diagnostic reagent  
PS Example; Table III, Page 16; 52pp; English.  
CC A novel ARD 1 protein includes an 18 kDa region that  
CC exhibits significant homology to known ADP-ribosylation factors  
CC (ARFs) and is called ARD 1 for ARF domain. cDNA was isolated from a  
CC human HL-60 lambda library screened with ARF 2B cDNA and a mixture of  
CC oligos denoted XARFC. The insert of Clone no. 76 was sequenced. The  
CC insert (bps 706-2365 Q79326) included an ORF (1207-1722) encoding  
CC an ARF domain of 172 AAs. Oligo J1R was used to screen a human  
CC fetal brain cDNA lambda ZAP library. Clones were found contg.  
CC nucleotides 7-1826 and 726-3225 of Q79326. In this sequence, about  
CC 1200 nts preceded the ARF region without a stop codon in the same  
CC ORF. To further characterise the 5' terminus of this cDNA, 5'-RACE  
CC was carried out with the poly A+ RNA from IMR-52 human  
CC neuroblastoma cells. The poly A+ RNA was reverse transcribed with  
CC primer JK721RC. The products were tailed and subcloned to PCR with  
CC primers SALAD and SALADT and JK723RII. TE was added to the PCR  
CC products and a second PCR amplification was carried out using  
CC primers SALAD and JKNOT. Following transfection of the reverse  
CC transcribed, PCR amplified sequences into competent DH5-alpha  
CC cells, clones corresp. to ARD 1 were isolated.  
SQ Sequence 35 BP; 4 A; 12 C; 11 G; 8 T;

Query Match 3.7%; Score 17; DB 13; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.17e+00;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 gtcgacccacgctccg 35  
|||||  
Qy 40 gtcgacccacgctccg 56

Search completed: Mon Mar 8 23:40:43 1999  
Job time : 314 secs.

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WORLD

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 23:41:01 1999; MasPar time 35.32 Seconds  
Tabular output not generated. 1148.278 Million cell updates/sec

Title: >US-09-206-040-1  
Description: (1-469) from US09206040A.seq  
Perfect Score: 465  
N.A. Sequence: 1 ttaacttcgagcgcgcaggt.....gatgatacatggaagatntt 469  
Comp: aattgaacgtcgnggtcca.....ctactatgtaacttcanna

Scoring table: TABLE jmetric  
Gap 60

Nmatch STD : Dbase 0; Query 0

Searched: 165359 seqs, 43243793 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-issued  
1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Statistics: Mean 6.835; Variance 2.301; scale 2.970

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description	Pred. No.
1	28	6.0	570	3	US-08-633- Sequence 1, Applicatio	1.25e-11
2	28	6.0	969	3	US-08-700- Sequence 1, Applicatio	1.25e-11
3	28	6.0	1023	3	US-08-785- Sequence 2, Applicatio	1.25e-11
4	28	6.0	1529	3	US-08-726- Sequence 1, Applicatio	1.25e-11
5	28	6.0	1581	2	US-08-383- Sequence 1, Applicatio	1.25e-11
6	28	6.0	1581	3	US-08-460- Sequence 1, Applicatio	1.25e-11
7	21	4.5	1257	2	US-08-487- Sequence 11, Applicatio	5.73e-05
8	21	4.5	2055	2	US-08-487- Sequence 3, Applicatio	5.73e-05
9	18	3.9	36	1	US-08-049- Sequence 20, Applicati	2.33e-02
10	18	3.9	36	1	US-08-312- Sequence 20, Applicati	2.33e-02
11	18	3.9	36	4	PCT-US94-0 Sequence 20, Applicatio	2.33e-02
12	18	3.9	1930	4	PCT-US95-0 Sequence 1, Applicatio	2.33e-02
13	18	3.9	1930	2	US-08-544- Sequence 1, Applicatio	2.33e-02
14	18	3.9	2721	5	5215881-2 Patent No. 5215881	2.33e-02
15	17	3.7	35	1	US-08-049- Sequence 21, Applicati	1.55e-01
16	17	3.7	35	1	US-08-312- Sequence 21, Applicati	1.55e-01
17	17	3.7	35	4	PCT-US94-0 Sequence 21, Applicati	1.55e-01
18	17	3.7	538	3	US-08-890- Sequence 1, Applicatio	1.55e-01
19	17	3.7	925	2	US-08-544- Sequence 3, Applicatio	1.55e-01
20	17	3.7	925	4	PCT-US95-0 Sequence 2, Applicatio	1.55e-01

21	17	3.7	1700	4	PCT-US95-0 Sequence 3, Applicatio	1.55e-01	
22	17	3.7	1983	1	US-08-073- Sequence 9, Applicatio	1.55e-01	
23	17	3.7	2288	3	US-08-568- Sequence 5, Applicatio	1.55e-01	
24	17	3.7	2606	3	US-08-568- Sequence 7, Applicatio	1.55e-01	
25	17	3.7	2710	2	US-08-487- Sequence 8, Applicatio	1.55e-01	
26	16	3.4	16	3	US-08-407- Sequence 44, Applicati	9.74e-01	
27	16	3.4	35	3	US-08-447- Sequence 77, Applicati	9.74e-01	
28	16	3.4	39	2	US-08-846- Sequence 11, Applicati	9.74e-01	
c	29	16	3.4	39	2	US-08-385- Sequence 11, Applicati	9.74e-01
c	29	16	3.4	39	2	US-08-385- Sequence 2, Applicatio	9.74e-01
c	30	16	3.4	925	4	PCT-US95-0 Sequence 3, Applicatio	9.74e-01
c	31	16	3.4	925	2	US-08-344- Sequence 3, Applicatio	9.74e-01
c	32	16	3.4	975	3	US-08-842- Sequence 9, Applicatio	9.74e-01
c	33	16	3.4	975	2	US-08-671- Sequence 9, Applicatio	9.74e-01
c	34	16	3.4	975	2	US-08-672- Sequence 9, Applicatio	9.74e-01
c	35	16	3.4	975	3	US-08-842- Sequence 9, Applicatio	9.74e-01
c	36	16	3.4	1264	3	US-08-758- Sequence 13, Applicatio	9.74e-01
c	37	16	3.4	1425	2	US-08-846- Sequence 1, Applicatio	9.74e-01
c	38	16	3.4	1425	2	US-08-385- Sequence 2, Applicatio	9.74e-01
c	39	16	3.4	1762	3	US-08-742- Sequence 1, Applicatio	9.74e-01
c	40	16	3.4	4010	3	US-08-785- Sequence 3, Applicatio	9.74e-01
c	41	16	3.4	4447	3	US-08-304- Sequence 3, Applicatio	9.74e-01
c	42	16	3.4	8540	4	PCT-US96-0 Sequence 12, Applicati	9.74e-01
c	43	16	3.4	8575	4	PCT-US92-0 Sequence 6, Applicatio	9.74e-01
c	44	16	3.4	10580	1	US-08-196- Sequence 1, Applicatio	9.74e-01
c	45	16	3.4	10596	4	PCT-US93-0 Sequence 15, Applicati	9.74e-01

## ALIGNMENTS

RESULT 1  
ID US-08-633-682-1 STANDARD; DNA; UNC; 570 BP.  
AC xxxxxx  
DT  
DE Sequence 1, Application US/08633682  
CC Sequence 1, Application US/08633682  
CC Patent No. 5840544  
CC GENERAL INFORMATION:  
CC APPLICANT: Hawkins, Phillip R.  
CC APPLICANT: Bandman, Olga  
CC APPLICANT: Murry, Lynn E.  
CC TITLE OF INVENTION: NOVEL RANTES HOMOLOG FROM PROSTATE  
CC NUMBER OF SEQUENCES: 5  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Incyte Pharmaceuticals, Inc.  
CC STREET: 3174 Porter Drive  
CC CITY: Palo Alto  
CC STATE: CA  
CC COUNTRY: U.S.  
CC ZIP: 94304  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FastSeq Version 1.5  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/633,682  
CC FILING DATE: Filed Herewith  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Luther, Barbara J  
CC REGISTRATION NUMBER: 33,954  
CC REFERENCE/DOCKET NUMBER: PF-0063 US  
CC TELEPHONE: 415-855-0555  
CC TELEFAX: 415-852-0195  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 570 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC IMMEDIATE SOURCE:  
CC LIBRARY: Prostate

CC CLONE: 836820  
SQ SEQUENCE 570 BP; 149 A; 155 C; 137 G; 129 T; 0 OTHER.

Query Match 6.0%; Score 28; DB 3; Length 570;  
Best Local Similarity 100.0%; Pred. No. 1.25e-11;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 59 GGAATTCGGGTGACCCAGCGTCG 86  
|||||  
Qy 29 ggaattccgggtgacccagcgctcg 56

RESULT 2  
ID US-08-700-637-1 STANDARD; DNA; UNC; 969 BP.  
AC xxxxxx

DE Sequence 1, Application US/08700637  
CC Sequence 1, Application US/08700637  
CC Patent No. 5854413

GENERAL INFORMATION:  
CC APPLICANT: Hawkins, Phillip R.  
CC APPLICANT: Stuart, Susan G.  
CC APPLICANT: Murry, Lynn E.  
CC TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON  
CC NUMBER OF SEQUENCES: 12  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Incyte Pharmaceuticals, Inc.  
CC STREET: 3174 Porter Drive  
CC CITY: Palo Alto  
CC STATE: CA  
CC COUNTRY: U.S.  
CC ZIP: 94304

COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FastSeq Version 1.5  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/700.637  
CC FILING DATE: Filed Herewith  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Luther, Barbara J.  
CC REGISTRATION NUMBER: 33,954  
CC REFERENCE/DOCKET NUMBER: PF-0065 US  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415-855-0555  
CC TELEFAX: 415-852-0195

INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 969 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC IMMEDIATE SOURCE:  
CC LIBRARY: COLNOT05  
CC CLONE: 775426

SQ SEQUENCE 969 BP; 163 A; 324 C; 280 G; 202 T; 0 OTHER.

Query Match 6.0%; Score 28; DB 3; Length 969;  
Best Local Similarity 100.0%; Pred. No. 1.25e-11;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 59 GGAATTCGGGTGACCCAGCGTCG 86  
|||||  
Qy 29 ggaattccgggtgacccagcgctcg 56

RESULT 3  
ID US-08-785-065-2 STANDARD; DNA; UNC; 1023 BP.  
AC xxxxxx

DE Sequence 2, Application US/08785065

CC Sequence 2, Application US/08785065  
CC Patent No. 5814451

GENERAL INFORMATION:  
CC APPLICANT: Bandman, Olga  
CC APPLICANT: Goli, Surya K.  
CC APPLICANT: Hillman, Jennifer L.  
CC TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE  
CC NUMBER OF SEQUENCES: 12  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Incyte Pharmaceuticals, Inc.  
CC STREET: 3174 Porter Drive  
CC CITY: Palo Alto  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 94304

COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette  
CC COMPUTER: IBM Compatible  
CC OPERATING SYSTEM: DOS  
CC SOFTWARE: FastSeq for Windows Version 2.0  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/785.065  
CC FILING DATE: Herewith  
CC CLASSIFICATION: 424  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER:  
CC FILING DATE:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Billings, Lucy J.  
CC REGISTRATION NUMBER: 36,749  
CC REFERENCE/DOCKET NUMBER: PF-0187 US  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 415-855-0555  
CC TELEFAX: 415-845-4166  
CC TELEX:

INFORMATION FOR SEQ ID NO: 2:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1023 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC IMMEDIATE SOURCE:  
CC LIBRARY:  
CC CLONE: Consensus

SQ SEQUENCE 1023 BP; 217 A; 270 C; 290 G; 246 T; 0 OTHER.

Query Match 6.0%; Score 28; DB 3; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 1.25e-11;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 GGAATTCGGGTGACCCAGCGTCG 81  
|||||  
Qy 29 ggaattccgggtgacccagcgctcg 56

RESULT 4  
ID US-08-726-575A-1 STANDARD; DNA; UNC; 1529 BP.  
AC xxxxxx

DE Sequence 1, Application US/08726575A  
CC Sequence 1, Application US/08726575A  
CC Patent No. 5834587

GENERAL INFORMATION:  
CC APPLICANT: Winnie Chan, Derk J. Bergsma,  
CC APPLICANT: Catherine E. Ellis  
CC TITLE OF INVENTION: A No. 5834587el G-Protein Coupled Receptor,  
CC TITLE OF INVENTION: HLTX11  
CC NUMBER OF SEQUENCES: 5  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: SmithKline Beecham Corporation  
CC STREET: 709 Swedeland Road, P.O. Box 1539  
CC CITY: King of Prussia  
CC STATE: PA



CC COUNTRY: USA  
CC ZIP: 19406-0939  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE  
CC COMPUTER: IBM 486  
CC OPERATING SYSTEM: WINDOWS FOR WORKGROUPS  
CC SOFTWARE: WORDPERFECT 5.1  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/726,575A  
CC FILING DATE: OCTOBER 8, 1996  
CC CLASSIFICATION: 514  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER:  
CC FILING DATE:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: William T. Han  
CC REGISTRATION NUMBER: 34,344  
CC REFERENCE/DOCKET NUMBER: ATG 50025  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 610 270 5219  
CC TELEFAX: 610 270 4026  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1529  
CC TYPE: Nucleic Acid  
CC STRANDEDNESS: Single  
CC TOPOLOGY: Linear  
CC ANTI-SENSE: NO  
CC SEQUENCE 1529 BP; 390 A; 374 C; 315 G; 450 T; 0 OTHER.  
SQ  
Query Match 6.0%; Score 28; DB 3; Length 1529;  
Best Local Similarity 100.0%; Pred. No. 1.25e-11;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 25 GGAATCCCGGTCGACCCACGCGTCG 52  
|||||  
QY 29 ggaattcccggtcgaccacggtccg 56  
RESULT 5  
ID US-08-383-756-1 STANDARD; DNA; UNC; 1581 BP.  
AC xxxxxx  
DT Sequence 1, Application US/08383756  
DE Sequence 1, Application US/08383756  
CC Patent No. 5654495  
CC GENERAL INFORMATION:  
CC APPLICANT: Debesh, Katayoon  
CC APPLICANT: Voelker, Toni Alois  
CC APPLICANT: Hawkins, Deborah  
CC APPLICANT: Davies, Huw Maelor  
CC TITLE OF INVENTION: Production of Myristate in Plant Cells  
CC NUMBER OF SEQUENCES: 17  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Calgene, Inc.  
CC STREET: 1920 Fifth Street  
CC CITY: Davis  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 95616  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB  
CC OPERATING SYSTEM: Macintosh  
CC SOFTWARE: Microsoft Word 5.1(a)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/383,756  
CC FILING DATE: 02-FEB-1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/261,695  
CC FILING DATE: 16-JUN-94  
CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US93/10814  
CC FILING DATE: 29-OCT-93  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: USSN 07/968,971  
CC FILING DATE: 30-OCT-92  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Elizabeth Lassen  
CC REGISTRATION NUMBER: 31,845  
CC NAME: Donna E. Scherer  
CC REGISTRATION NUMBER: 34,719  
CC NAME: Carl J. Schwedler  
CC REGISTRATION NUMBER: 36,924  
CC REFERENCE/DOCKET NUMBER: CGNE 111  
CC TELEPHONE: (916) 753-6313  
CC TELEFAX: (916) 753-1510  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1581 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA to mRNA  
CC SEQUENCE 1581 BP; 418 A; 356 C; 410 G; 397 T; 0 OTHER.  
SQ  
Query Match 6.0%; Score 28; DB 2; Length 1581;  
Best Local Similarity 100.0%; Pred. No. 1.25e-11;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 54 GGAATCCCGGTCGACCCACGCGTCG 81  
|||||  
QY 29 ggaattcccggtcgaccacggtccg 56  
RESULT 6  
ID US-08-460-898-1 STANDARD; DNA; UNC; 1581 BP.  
AC xxxxxx  
DT Sequence 1, Application US/08460898  
DE Sequence 1, Application US/08460898  
CC Patent No. 5850022  
CC GENERAL INFORMATION:  
CC APPLICANT: Debesh, Katayoon  
CC APPLICANT: Voelker, Toni Alois  
CC APPLICANT: Hawkins, Deborah  
CC APPLICANT: Davies, Huw Maelor  
CC TITLE OF INVENTION: Production of Myristate in Plant Cells  
CC NUMBER OF SEQUENCES: 17  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Calgene, Inc.  
CC STREET: 1920 Fifth Street  
CC CITY: Davis  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 95616  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB  
CC OPERATING SYSTEM: Macintosh  
CC SOFTWARE: Microsoft Word 5.1(a)  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/460,898  
CC FILING DATE: 05-JUN-1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/383,756  
CC FILING DATE: 02-FEB-1995  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: 08/261,695  
CC FILING DATE: 16-JUN-94  
CC CLASSIFICATION: 435

CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US93/10814  
CC FILING DATE: 29-OCT-93  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: USSN 07/968,971  
CC FILING DATE: 30-OCT-92  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Elizabeth Lassen  
CC REGISTRATION NUMBER: 31,845  
CC NAME: Donna E. Scherer  
CC REGISTRATION NUMBER: 34,719  
CC NAME: Carl J. Schwedler  
CC REGISTRATION NUMBER: 36,924  
CC REFERENCE/DOCKET NUMBER: CGNE 111-1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (916) 753-6313  
CC TELEFAX: (916) 753-1510  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1581 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cdna to mRNA  
CC SEQUENCE 1581 BP; 418 A; 356 C; 410 G; 397 T; 0 OTHER.  
Query Match 6.0%; Score 28; DB 3; Length 1581;  
Best Local Similarity 100.0%; Pred.No. 1.25e-11;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 54 GGAATCCCGGTCGACCCAGCGTCGC 81  
QY 29 ggaattcccggtcgaccacgcgctccg 56  
RESULT 7  
ID US-08-487-748A-11 STANDARD; DNA; UNC; 1257 BP.  
AC xxxxxx  
DT  
DE Sequence 11, Application US/08487748A  
CC Sequence 11, Application US/08487748A  
CC Patent No. 5721351  
CC GENERAL INFORMATION:  
CC APPLICANT: Levinson, Douglas A.  
CC TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
CC TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
CC NUMBER OF SEQUENCES: 23  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Pennie & Edmonds  
CC STREET: 1155 Avenue of the Americas  
CC CITY: New York  
CC STATE: New York  
CC COUNTRY: U.S.A.  
CC ZIP: 10036-2711  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/487,748A  
CC FILING DATE: 07-JUN-1995  
CC CLASSIFICATION: 536  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Pennie & Edmonds  
CC STREET: 1155 Avenue of the Americas  
CC CITY: New York  
CC STATE: New York  
CC COUNTRY: U.S.A.  
CC ZIP: 10036-2711  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/487,748A  
CC FILING DATE: 07-JUN-1995  
CC CLASSIFICATION: 536  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Coruzzi, Laura A.  
CC REGISTRATION NUMBER: 30,742  
CC REFERENCE/DOCKET NUMBER: 7853-023  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (212) 790-9090  
CC TELEFAX: (212) 869-8864/9741  
CC TELEX: 66141 PENNIE

CC INFORMATION FOR SEQ ID NO: 11:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1257 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: unknown  
CC MOLECULE TYPE: DNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 22, 1137  
CC SEQUENCE 1257 BP; 323 A; 357 C; 323 G; 253 T; 1 OTHER.  
Query Match 4.5%; Score 21; DB 2; Length 1257;  
Best Local Similarity 100.0%; Pred.No. 5.73e-05;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 CCGGGTCGACCCAGCGTCGC 21  
QY 36 ccgggtcgaccacgcgctccg 56  
RESULT 8  
ID US-08-487-748A-3 STANDARD; DNA; UNC; 2055 BP.  
AC xxxxxx  
DT  
DE Sequence 3, Application US/08487748A  
CC Sequence 3, Application US/08487748A  
CC Patent No. 5721351  
CC GENERAL INFORMATION:  
CC APPLICANT: Levinson, Douglas A.  
CC TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
CC TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS  
CC NUMBER OF SEQUENCES: 23  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Pennie & Edmonds  
CC STREET: 1155 Avenue of the Americas  
CC CITY: New York  
CC STATE: New York  
CC COUNTRY: U.S.A.  
CC ZIP: 10036-2711  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/487,748A  
CC FILING DATE: 07-JUN-1995  
CC CLASSIFICATION: 536  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Coruzzi, Laura A.  
CC REGISTRATION NUMBER: 30,742  
CC REFERENCE/DOCKET NUMBER: 7853-023  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (212) 790-9090  
CC TELEFAX: (212) 869-8864/9741  
CC TELEX: 66141 PENNIE  
CC INFORMATION FOR SEQ ID NO: 3:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 2055 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: unknown  
CC MOLECULE TYPE: DNA  
CC FEATURE:  
CC NAME/KEY: CDS  
CC LOCATION: 496, 1509  
CC SEQUENCE 2055 BP; 623 A; 460 C; 415 G; 557 T; 0 OTHER.  
Query Match 4.5%; Score 21; DB 2; Length 2055;  
Best Local Similarity 100.0%; Pred.No. 5.73e-05;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CCGGTCGACCCAGCGTCG 21
Qy 36 ccgggtcgaccacgcgtccg 56

RESULT 9
ID US-08-049-473-20 STANDARD; DNA; UNC; 36 BP.
AC xxxxxx
DE Sequence 20, Application US/08049473
CC Sequence 20, Application US/08049473
CC Patent No. 5386021
CC GENERAL INFORMATION:
CC APPLICANT: Moss, Joel
CC APPLICANT: Mishima, Koichi
CC APPLICANT: Nightingale, Maria
CC APPLICANT: Tsuchiya, Mikako
CC TITLE OF INVENTION: A MAMMALIAN GUANIN NUCLEOTIDE BINDING
CC TITLE OF INVENTION: PROTEIN WITH AN ADP-RYBOSYLATION FACTOR DOMAIN
CC NUMBER OF SEQUENCES: 34
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
CC STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CC CITY: NEWPORT BEACH
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92660
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/049,473
CC FILING DATE: 19-APR-1993
CC CLASSIFICATION: 436
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/049,473
CC FILING DATE: 19-APR-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fuller, Michael L.
CC REGISTRATION NUMBER: 36,516
CC REFERENCE/DOCKET NUMBER: NIH050.001DVI
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-235-8550
CC TELEFAX: 619-235-0176
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 36 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cdna
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC SEQUENCE 36 BP; 4 A; 12 C; 11 G; 9 T; 0 OTHER.

Query Match 3.9%; Score 18; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.33e-02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 GTCGACCCAGCGTCG 36
Qy 40 gtcgaccacgcgtccg 57

RESULT 11
ID PCT-US94-04190-20 STANDARD; DNA; UNC; 36 BP.
AC xxxxxx
DE Sequence 20, Application PC/TUS9404190
CC Sequence 20, Application PC/TUS9404190
CC GENERAL INFORMATION:
CC APPLICANT: The Government of the United States of America
CC APPLICANT: as represented by the Secretary, Department
CC APPLICANT: of Health and Human Services
CC TITLE OF INVENTION: A MAMMALIAN GUANIN NUCLEOTIDE BINDING
CC TITLE OF INVENTION: PROTEIN WITH AN ADP-RYBOSYLATION FACTOR DOMAIN
CC NUMBER OF SEQUENCES: 34
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
CC STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CC CITY: NEWPORT BEACH
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92660
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
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Db 1 CCGGTCGACCCAGCGTCG 21
Qy 36 ccgggtcgaccacgcgtccg 56

RESULT 9
ID US-08-049-473-20 STANDARD; DNA; UNC; 36 BP.
AC xxxxxx
DE Sequence 20, Application US/08049473
CC Sequence 20, Application US/08049473
CC Patent No. 5386021
CC GENERAL INFORMATION:
CC APPLICANT: Moss, Joel
CC APPLICANT: Mishima, Koichi
CC APPLICANT: Nightingale, Maria
CC APPLICANT: Tsuchiya, Mikako
CC TITLE OF INVENTION: A MAMMALIAN GUANIN NUCLEOTIDE BINDING
CC TITLE OF INVENTION: PROTEIN WITH AN ADP-RYBOSYLATION FACTOR DOMAIN
CC NUMBER OF SEQUENCES: 34
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR
CC STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CC CITY: NEWPORT BEACH
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 92660
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/049,473
CC FILING DATE: 19-APR-1993
CC CLASSIFICATION: 436
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/049,473
CC FILING DATE: 19-APR-1993
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Fuller, Michael L.
CC REGISTRATION NUMBER: 36,516
CC REFERENCE/DOCKET NUMBER: NIH050.001CP1
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 619-235-8550
CC TELEFAX: 619-235-0176
CC INFORMATION FOR SEQ ID NO: 20:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 36 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cdna
CC HYPOTHETICAL: NO
CC ANTI-SENSE: NO
CC SEQUENCE 36 BP; 4 A; 12 C; 11 G; 9 T; 0 OTHER.

Query Match 3.9%; Score 18; DB 1; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.33e-02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 GTCGACCCAGCGTCG 36
Qy 40 gtcgaccacgcgtccg 57

RESULT 10
ID US-08-312-648-20 STANDARD; DNA; UNC; 36 BP.
AC xxxxxx
DE Sequence 20, Application US/08312648
CC Sequence 20, Application US/08312648
CC Patent No. 5514600
CC GENERAL INFORMATION:
CC APPLICANT: Moss, Joel
CC APPLICANT: Mishima, Koichi
```

CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US94/04190  
CC FILING DATE:  
CC CLASSIFICATION:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Fuller, Michael L.  
CC REGISTRATION NUMBER: 36,516  
CC REFERENCE/DOCKET NUMBER: NIH050.001QPC  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619-235-8550  
CC TELEFAX: 619-235-0176  
CC INFORMATION FOR SEQ ID NO: 20:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 36 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
CC SEQUENCE 36 BP; 4 A; 12 C; 11 G; 9 T; 0 OTHER.

Query Match 3.9%; Score 18; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.33e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 19 GTCGACCCACGCGTCG 36  
Qy 40 gtcgacccacgcgtcgt 57

RESULT 12  
ID PCT-US95-07874-1 STANDARD; DNA; UNC; 1930 BP.  
AC xxxxxx

DE Sequence 1, Application PC/TUS9507874  
CC Sequence 1, Application PC/TUS9507874  
CC GENERAL INFORMATION:

CC APPLICANT:  
CC TITLE OF INVENTION: Method for Identifying Nucleic Acids Encoding c-fos Promoter  
CC NUMBER OF SEQUENCES: 2  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: Apple Macintosh  
CC OPERATING SYSTEM: Macintosh 7.1  
CC SOFTWARE: Microsoft Word 5.1a  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: PCT/US95/07874  
CC FILING DATE: June-1995

CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US 08/272,412  
CC FILING DATE: 8-JUL-1994  
CC INFORMATION FOR SEQ ID NO: 1:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 1930 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: double  
CC TOPOLOGY: linear  
CC SEQUENCE 1930 BP; 524 A; 487 C; 404 G; 515 T; 0 OTHER.

Query Match 3.9%; Score 18; DB 4; Length 1930;  
Best Local Similarity 100.0%; Pred. No. 2.33e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 GGTGACCCACGCGTCG 72  
Qy 39 ggtgacccacgcgtcgcg 56

RESULT 13

ID US-08-544-900-1 STANDARD; DNA; UNC; 1930 BP.  
AC xxxxxx

DE Sequence 1, Application US/08544900  
CC Sequence 1, Application US/08544900  
CC Patent No. 5736331

CC GENERAL INFORMATION:  
CC APPLICANT: Lin, Stanley L.  
CC APPLICANT: Rothofsky, Marnie Lynn  
CC TITLE OF INVENTION: Method for Identifying Nucleic  
CC TITLE OF INVENTION: Acids Encoding c-fos Promoter  
CC NUMBER OF SEQUENCES: 3  
CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Schering-Plough Corporation  
CC ADDRESSEE: Patent Department K-6-1 (1990)  
CC STREET: 2000 Galloping Hill Road  
CC CITY: Kenilworth  
CC STATE: New Jersey  
CC COUNTRY: USA

CC ZIP: 07033-0530

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: Apple Macintosh

CC OPERATING SYSTEM: Macintosh 7.1

CC SOFTWARE: Microsoft Word 5.1a

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/544,900

CC FILING DATE:

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/272,412

CC FILING DATE: 8-JUL-1994

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Thompson, Paul A.

CC REGISTRATION NUMBER: 35,385

CC REFERENCE/DOCKET NUMBER: OC0439K

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 908 298 5150

CC TELEFAX: 908 298 5388

CC TELEX:

CC INFORMATION FOR SEQ ID NO: 1:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 1930 base pairs

CC TYPE: nucleic acid

CC STRANDEDNESS: double

CC TOPOLOGY: linear

CC MOLECULE TYPE: cDNA

CC SEQUENCE 1930 BP; 524 A; 487 C; 404 G; 515 T; 0 OTHER.

Query Match 3.9%; Score 18; DB 2; Length 1930;  
Best Local Similarity 100.0%; Pred. No. 2.33e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 55 GGTGACCCACGCGTCG 72

Qy 39 ggtgacccacgcgtcgcg 56

RESULT 14

ID 5215881-2 STANDARD; DNA; UNC; 2948 BP.

AC xxxxxx

DT 01-JAN-1900

DE Patent No. 5215881.

CC Patent No. 5215881

CC APPLICANT: CHEUNG, ANDREW K.

CC TITLE OF INVENTION: PSEUDORABIES DIAGNOSIS PROBES

CC NUMBER OF SEQUENCES: 3

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/07/537,855

CC FILING DATE: 13-JUN-1990

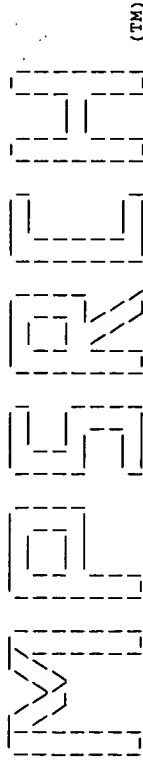
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CC LENGTH: 2721  
SQ Sequence 2948 BP; 428 A; 1007 C; 1017 G; 269 T; 227 other;  
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Best Local Similarity 100.0%; Pred. No. 2.33e-02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 141 CTCCTTTTCCCCCCCCCT 158  
Cp 96 ctctcttccccccct 79  
RESULT 15  
ID US-08-049-473-21 STANDARD; DNA; UNC; 35 BP.  
AC xxxxxx  
DT  
DE Sequence 21, Application US/08049473  
CC Sequence 21, Application US/08049473  
CC Patent No. 5386021  
CC GENERAL INFORMATION:  
CC APPLICANT: Moss, Joel  
CC APPLICANT: Mishima, Koichi  
CC APPLICANT: Nightingale, Maria  
CC APPLICANT: Tsuchiya, Mikako  
CC TITLE OF INVENTION: A MAMMALIAN GUANIN NUCLEOTIDE BINDING  
CC TITLE OF INVENTION: PROTEIN WITH AN ADP-RYBOSYLATION FACTOR DOMAIN  
CC NUMBER OF SEQUENCES: 34  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: KNOBBE, MARTENS, OLSON AND BEAR  
CC STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR  
CC CITY: NEWPORT BEACH  
CC STATE: CA  
CC COUNTRY: USA  
CC ZIP: 92660  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/049,473  
CC FILING DATE: 19930419  
CC CLASSIFICATION: 436  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Fuller, Michael L.  
CC REGISTRATION NUMBER: 36,516  
CC REFERENCE/DOCKET NUMBER: NIH050.001CPI  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 619-235-8550  
CC TELEFAX: 619-235-0176  
CC INFORMATION FOR SEQ ID NO: 21:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 35 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: cDNA  
CC HYPOTHETICAL: NO  
CC ANTI-SENSE: NO  
SQ SEQUENCE 35 BP; 4 A; 12 C; 11 G; 8 T; 0 OTHER.  
Query Match 3.7%; Score 17; DB 1; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.55e-01;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 19 GTCGACCCACGGCTCG 35  
Qy 40 gtcgaccacgcgctccg 56

Search completed: Mon Mar 8 23:42:51 1999  
Job time : 110 secs.

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 (TM)

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MParch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 23:10:19 1999; MasPar time 622.20 seconds  
 Tabular output not generated. 1349.844 Million cell updates/sec

Title: >US-09-206-040-1  
 Description: (1-469) from US09206040A.seq  
 Perfect Score: 465  
 N.A. Sequence: 1 ttaactgtcagcgnccaggt.....gatgatacattgaagatnt 469  
 Comp: attggaactgcgnggcca.....ctactatgtaacttctanna

Scoring table: TABLE jmetric  
 Gap 60

Nmatch STD : Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%  
 Listing first 45 summaries

Database: emb1-est56  
 Database: 1:em\_est1 2:em\_gss1 3:em\_gss2 4:em\_gss3  
 genbank-est109  
 5:gb\_est1 6:gb\_est10 7:gb\_est11 8:gb\_est12 9:gb\_est13  
 10:gb\_est14 11:gb\_est15 12:gb\_est16 13:gb\_est17  
 14:gb\_est18 15:gb\_est19 16:gb\_est2 17:gb\_est20  
 18:gb\_est21 19:gb\_est3 20:gb\_est4 21:gb\_est5 22:gb\_est6  
 23:gb\_est7 24:gb\_est8 25:gb\_est9 26:gb\_gss1 27:gb\_gss2  
 28:gb\_gss3 29:gb\_gss4

Statistics: Mean 8.493; Variance 1.124; scale 7.553

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being printed,  
 and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
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2	29	6.2	214	21	T18296	5C06d02-t7 membrane-fr
3	29	6.2	331	21	T18319	5C06h03-t7 membrane-fr
4	29	6.2	407	21	T18280	5C06a03-t7 membrane-fr
5	29	6.2	439	21	T18310	5C06g03-t7 membrane-fr
6	29	6.2	589	9	HS299396	Homo sapiens mRNA; exp
7	28	6.0	113	21	T18257	5C01e04-t7 membrane-fr
8	28	6.0	114	21	T18320	5C06h05-t7 membrane-fr
9	28	6.0	163	21	T18683	5C04E02-T7 membrane-fr
10	28	6.0	184	21	T18394	5C06c10-t7 membrane-fr
11	28	6.0	221	21	T18691	5C04F02-T7 membrane-fr
12	28	6.0	340	23	HSU46345	Human clone xs359 mRNA
13	28	6.0	350	23	HSU46346	Human clone xs360 mRNA

14	28	6.0	360	23	HSU46350	Human clone xs366 mRNA	1.72e-26
15	28	6.0	386	21	T18713	5C04G09-T7 membrane-fr	1.72e-26
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17	28	6.0	400	23	HSU46349	Human clone xs363 mRNA	1.72e-26
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 ACCESSION T18698  
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 KEYWORDS EST.  
 SOURCE maize.  
 ORGANISM Zea mays.  
 Eukaryotes; Mitochondrial eukaryotes; Viridiplantae;  
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 REFERENCE 1 (bases 1 to 568)  
 AUTHORS Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,  
 Helentjaris, T., Baysdorfer, C., Almira, E., Perl, R., Habben, J. and  
 Larkins, B.  
 TITLE Partial sequencing and mapping of clones from two maize cDNA  
 libraries  
 JOURNAL Plant Mol. Biol. 26, 1085-1101 (1994)  
 MEDLINE 95111093  
 COMMENT Contact: The Maize cDNA Project

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 fax: 904-392-4072  
 E-mail: robferl@nervm.nerdc.ufl.edu

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                     /clone="5C04F08"
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DEFINITION 5C06d02-t7 membrane-free polysomes from endospem Zea mays cDNA
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REFERENCE 1 (bases 1 to 214)
          Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T.,
          Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and
          Larkins,B.
          Partial sequencing and mapping of clones from two maize cDNA
          libraries
          Plant Mol. Biol. 26, 1085-1101 (1994)
MEDLINE 95111093
COMMENT

```

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                     adaptors were added to the ends, the ds-cDNAs were then
                     digested with NotI and size-selected. These were
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ACCESSION clone 5C06h03 5' end similar to ribosomal protein S8, mRNA
NID T18319
KEYWORDS EST.
SOURCE zeamays
ORGANISM Zea mays
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REFERENCE 1 (bases 1 to 331)
          Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T.,
          Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and
          Larkins,B.
          Partial sequencing and mapping of clones from two maize cDNA
          libraries
          Plant Mol. Biol. 26, 1085-1101 (1994)
JOURNAL

```



MEDLINE 95111093  
COMMENT

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E-mail: robferl@nervm.nerdc.ufl.edu

FEATURES  
Seq primer: T7.  
Location/Qualifiers  
1. .331  
/organism="Zea mays"  
/strain="W64A2"

/note="Vector: Ziplox; Site.1: SalI; Site.2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo- dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA Pol. SalI adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the Ziplox phage vector, excised as plasmids, and then individually analyzed."

/db\_xref="taxon:4577"

/clone="5c06h03"

/clone\_lib="membrane-free polysomes from endosperm"

/lab\_host="DH10B"

<1. .>331 81 a 78 c 103 g 57 t 12 others

BASE COUNT  
ORIGIN

Query Match 6.2%; Score 29; DB 21; Length 331;  
Best Local Similarity 100.0%; Pred. No. 8.16e-29;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 GGAATTCGCGGTGACCCACGCGTCGCT 37  
|||  
QY 29 ggaattccgcggtcgcacccgcgctcgt 57

RESULT 4  
LOCUS T18280 407 bp mRNA EST 17-OCT-1996  
DEFINITION 5c06h03-t7 membrane-free polysomes from endosperm Zea mays cDNA  
T18280  
ACCESSION 5c06h03 5' end, mRNA sequence.  
NID 9463313  
KEYWORDS EST.  
SOURCE maize.  
ORGANISM Zea mays  
Eukaryotae; mitochondrial eukaryotes; Vitidiplantae;  
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;

REFERENCE  
AUTHORS

Lilipalsida; Pales; Poaceae; Zea.  
1 (bases 1 to 407)  
Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T.,  
Helentjaris,T., Baysdorfer,C., Almirá,E., Ferl,R., Habben,J. and  
Larkin,B.

TITLE Partial sequencing and mapping of clones from two maize cDNA  
libraries

JOURNAL Plant Mol. Biol. 26, 1085-1101 (1994)  
MEDLINE 95111093

COMMENT

Contact: The Maize cDNA Project

Helentjaris TG (Primary contact)  
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FEATURES  
Seq primer: T7.  
Location/Qualifiers  
1. .407  
/organism="Zea mays"  
/strain="W64A2"

/note="Vector: Ziplox; Site.1: SalI; Site.2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo- dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA Pol. SalI adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the Ziplox phage vector, excised as plasmids, and then individually analyzed."

/db\_xref="taxon:4577"

/clone="5c06a03"

/clone\_lib="membrane-free polysomes from endosperm"

/lab\_host="DH10B"

BASE COUNT 113 a 80 c 95 g 119 t  
ORIGIN

Query Match 6.2%; Score 29; DB 21; Length 407;  
Best Local Similarity 100.0%; Pred. No. 8.16e-29;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 7 GGAATTCGCGGTGACCCACGCGTCGCT 35  
|||  
QY 29 ggaattccgcggtcgcacccgcgctcgt 57

RESULT 5  
LOCUS T18310 439 bp mRNA EST 17-OCT-1996  
DEFINITION 5c06g03-t7 membrane-free polysomes from endosperm Zea mays cDNA

ACCESSION clone 5c06g03 5' end, mRNA sequence.  
 T18310  
 MID 9463343  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays  
 Eukaryote; mitochondrial eukaryotes; Viridiplantae;  
 Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;  
 Liliopsida; Poales; Poaceae; Zea.  
 1 (bases 1 to 439)  
 REFERENCE Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,  
 Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habb, J., and  
 Larkins, B.  
 TITLE Partial sequencing and mapping of clones from two maize CDNA  
 libraries  
 JOURNAL Plant Mol. Biol. 26, 1085-1101 (1994)  
 MEDLINE 95111093  
 COMMENT Contact: The Maize cDNA Project

Helentjaris, TG (primary contact)  
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 University of Arizona  
 Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721  
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 fax: 602-621-7186  
 E-mail: helentjaris@cit.arizona.edu  
 Chris Baysdorfer  
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 California State University, Hayward  
 Hayward, CA 94542  
 ph: 510-881-3459  
 fax: 510-727-2035  
 E-mail: cbaysdorfer@csuhayward.edu  
 Rob Ferl  
 Interdisciplinary Center for Biotechnology Research  
 DNA Sequencing Core  
 University of Florida  
 P.O. Box 100695  
 Gainesville, FL 32611-0695  
 ph: 904-392-1928, ext. 301  
 fax: 904-392-4072  
 E-mail: robferl@nerc.ufl.edu

FEATURES  
 source

Seq primer: T7.  
 Location/Qualifiers  
 1..439  
 /organism="Zea mays"  
 /strain="W64A2"  
 /note="Vector: Ziplox; Site\_1: SalI; Site\_2: NotI; ds-cDNA  
 was prepared from oligo-dT selected mRNA by priming with a  
 NotI oligo- dT oligomer and then adding the second strand  
 to RNase-nicked DNA:RNA hybrid with DNA Pol. I. SalI  
 adaptors were added to the ends, the ds-cDNAs were then  
 digested with NotI and size selected. These were  
 directionally-cloned into the Ziplox phage vector, excised  
 as plasmids, and then individually analyzed."  
 /db\_xref="taxon:4577"  
 /clone="5c06g03"  
 /clone.lib="membrane-free polysomes from endosperm"  
 /lab.host="DH10B"  
 <1..>439  
 108 a 123 c 101 g 96 t 11 others  
 MRNA  
 BASE COUNT  
 ORIGIN

Query Match 6.2%; Score 29; DB 21; Length 439;  
 Best Local Similarity 100.0%; Pred. No. 8.16e-29;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 13 GGAATTCGGGGTCGACCCGCGTCGCT 41  
 ||||||||||||||||||||||||||||  
 Oy 29 ggaattccgggctcgaccacgcgctcgt 57  
 RESULT 6  
 LOCUS HS299396 589 bp DNA EST 19-SEP-1997  
 DEFINITION Homo sapiens mRNA; expressed sequence tag; clone DKFZphamy1\_1c11,  
 3' read, mRNA sequence.  
 ACCESSION 299396  
 MID g2415636  
 KEYWORDS EST; expressed sequence tag.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 589)  
 AUTHORS Korn, B., Mleemann, S., Ebert, L. and Poustka, A.  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 589)  
 AUTHORS Korn, B.  
 TITLE Direct Submission  
 JOURNAL Submitted (11-SEP-1997) Korn B., Institution Molekulare  
 Genomanalyse, Deutsches Krebsforschungszentrum Heidelberg, Im  
 Neuenheimer Feld 506, D-69120 Heidelberg, FRG  
 LOCATION/Qualifiers  
 1..589  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone.lib="DKFZphamy1"  
 /clone="DKFZphamy1\_1c11"  
 /tissue\_type="amygdala"  
 /dev\_stage="adult"

BASE COUNT 161 a 156 c 151 g 120 t 1 others  
 ORIGIN

Query Match 6.2%; Score 29; DB 9; Length 589;  
 Best Local Similarity 100.0%; Pred. No. 8.16e-29;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 398 ACGGACGGGTGGGTGACCCGCGAATTC 426  
 Cp 57 acggacgggtggtcgaccgcggaattcc 29  
 ||||||||||||||||||||||||||||

RESULT 7  
 LOCUS T18257 113 bp mRNA EST 17-OCT-1996  
 DEFINITION Sc01e04-t7 membrane-free polysomes from endosperm Zea mays CDNA  
 clone 5c01e04 5' end, mRNA sequence.  
 ACCESSION T18257  
 MID 9463280  
 KEYWORDS EST.  
 SOURCE Zea mays.  
 ORGANISM Zea mays  
 Eukaryote; mitochondrial eukaryotes; Viridiplantae;  
 Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;  
 Liliopsida; Poales; Poaceae; Zea.  
 1 (bases 1 to 113)  
 REFERENCE Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,  
 Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habb, J., and  
 Larkins, B.  
 TITLE Partial sequencing and mapping of clones from two maize CDNA  
 libraries  
 JOURNAL Plant Mol. Biol. 26, 1085-1101 (1994)  
 MEDLINE 95111093  
 COMMENT Contact: The Maize cDNA Project

Helentjaris, TG (primary contact)  
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 Fax: 602-621-7186  
 E-mail: helnjars@ccit.arizona.edu

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 Hayward, CA 94542  
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 Fax: 510-727-2035  
 E-mail: cbaysdor@esl.csuhayward.edu

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 DNA Sequencing Core  
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 Gainesville, FL 32611-0695  
 Ph: 904-392-1928, ext. 301  
 Fax: 904-392-4072  
 E-mail: robferl@nervm.nerdc.ufl.edu

FEATURES  
 Source Location/Qualifiers  
 1. .113  
 /organism="Zea mays"  
 /strain="W64A2"  
 /note="Vector: Ziplox; Site\_1: SalI; Site\_2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA Pol. SalI adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the Ziplox phage vector, excised as plasmids, and then individually analyzed."  
 /db\_xref="taxon:4577"  
 /clone\_1fb="5c01e04"  
 /lab\_host="DH10B"  
 /lab\_host="DH10B"

BASE COUNT  
 ORIGIN  
 mRNA  
 29 a 29 c 33 g 22 t

Query Match 6.0%; Score 28; DB 21; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 1.72e-26;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 GGAATCCCGGTCGACCGCGTCG 39  
 ||||||||||||||||||||||||||||  
 29 ggaattcccggtcgaccacgcgtccg 56

RESULT 8  
 LOCUS T18320 114 bp mRNA EST 17-OCT-1996  
 DEFINITION 5c06h05-t7 membrane-free polysomes from endosperm Zea mays cDNA  
 clone 5c06h05 5' end, mRNA sequence.  
 ACCESSION T18320  
 NID 9463353  
 KEYWORDS EST.  
 SOURCE maize.  
 ORGANISM Zea mays

REFERENCE  
 AUTHORS Eukaryotae; mitochondrial eukaryotes; Viridiplantae;  
 Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;  
 Liliopsida; Poales; Poaceae; Zea.  
 1 (bases 1 to 114)  
 Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,  
 Helentjaris, T., Baysdorfer, C., Almirante, E., Ferl, R., Hadden, J., and  
 Larkins, B.  
 TITLE Partial sequencing and mapping of clones from two maize cDNA  
 libraries  
 JOURNAL Plant Mol. Biol. 26, 1085-1101 (1994)  
 MEDLINE 95111093

## COMMENT

Contact: The Maize cDNA Project

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 Fax: 602-621-7186  
 E-mail: helnjars@ccit.arizona.edu

Chris Baysdorfer  
 Department of Biological Sciences, School of Science  
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 Hayward, CA 94542  
 Ph: 510-881-3459  
 Fax: 510-727-2035  
 E-mail: cbaysdor@esl.csuhayward.edu

Rob Ferl  
 Interdisciplinary Center for Biotechnology Research  
 DNA Sequencing Core  
 University of Florida  
 P.O. Box 100695  
 Gainesville, FL 32611-0695  
 Ph: 904-392-1928, ext. 301  
 Fax: 904-392-4072  
 E-mail: robferl@nervm.nerdc.ufl.edu

FEATURES  
 Source Location/Qualifiers  
 1. .114  
 /organism="Zea mays"  
 /strain="W64A2"  
 /note="Vector: Ziplox; Site\_1: SalI; Site\_2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA Pol. SalI adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the Ziplox phage vector, excised as plasmids, and then individually analyzed."  
 /db\_xref="taxon:4577"  
 /clone\_1fb="5c06h05"  
 /lab\_host="DH10B"  
 /lab\_host="DH10B"

BASE COUNT  
 ORIGIN  
 mRNA  
 24 a 33 c 27 g 28 t 2 others

Query Match 6.0%; Score 28; DB 21; Length 114;  
 Best Local Similarity 100.0%; Pred. No. 1.72e-26;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 10 GGAATCCCGGTCGACCGCGTCG 37  
 ||||||||||||||||||||||||||||  
 29 ggaattcccggtcgaccacgcgtccg 56

RESULT 9  
 LOCUS T18683 163 bp mRNA EST 17-OCT-1996  
 DEFINITION 5c04E02-T7 membrane-free polysomes from endosperm Zea mays cDNA  
 clone 5c04E02 5' end, mRNA sequence.  
 ACCESSION T18683  
 NID 9485613  
 KEYWORDS EST.  
 SOURCE maize.  
 ORGANISM Zea mays

Eukaryotae; mitochondrial eukaryotes; Viridiplantae;  
 Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;  
 Liliopsida; Poales; Poaceae; Zea.

**REFERENCE**

(bases 1 to 163)

**AUTHORS**

Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T., Helentjaris,T., Baysdorfer,C., Almita,E., Ferl,R., Habben,J. and Larkins,J.

**TITLE**

Partial sequencing and mapping of clones from two maize cDNA libraries

**JOURNAL MEDLINE**

Plant Mol. Biol. 26, 1085-1101 (1994)  
95111093

**COMMENT**

Contact: The Maize CDNA Project  
  
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Dept. of Plant Sciences  
University of Arizona  
Dept. of Plant Sciences, University of Arizona, Tucson, AZ, 85721  
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fax: 602-621-7186  
E-mail: helnjars@cclt.arizona.edu  
  
Chris Baysdorfer  
Department of Biological Sciences, School of Science  
California State University, Hayward  
Hayward, CA 94542  
ph: 510-881-3459  
fax: 510-727-2035  
E-mail: cbaysdore@s1.csuhayward.edu  
  
Rob Ferl  
Interdisciplinary Center for Biotechnology Research  
DNA Sequencing Core  
University of Florida  
P.O. Box 100695  
Gainesville, FL 32611-0695  
ph: 904-392-1928, ext. 301  
fax: 904-392-4072  
E-mail: roberf@herm.ncrc.ufl.edu

**FEATURES**

Seq primer: T7.  
Location/Qualifiers

1..163  
    ~~/organism="Zea mays"~~  
    ~~/strain="W64A2"~~  
    ~~/note="Vector: Ziplox; Site\_1: SalI; Site\_2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo- dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA Pol. I. Salt adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the Ziplox phage vector, excised as plasmids, and then individually analyzed."~~  
    ~~/db\_xref="taxon:4577"~~  
    ~~/clone\_id="membrane-free polysomes from endosperm"~~  
    ~~/lab\_host="DHIOB"~~  
    <1..>163

RNASE COUNT     92 A       23 C       27 G       16 t           5 others  
ORIGIN

MATCHES

Query Match          6.0%; Score 28; DB 21; Length 163;  
Best Local Similarity 100.0%; Pred. Mismatch 0; Indels 0; Gaps 0;

DATABASE

DB     24 GGAAATCCCGGGTCGACGCCAGCCTCG 51  
      |||||  
QY    29 ggaattcccgggctgcagcccacgacctcgg 56

LOCUS     10       T18294           184 bp       RNASE       EST       17-OCT-1996  
DEFINITION     Sc06ClO-t7 membrane-free polysomes from endosperm Zea mays cDNA clone Sc06ClO 5' end, mRNA sequence.

DB	10	GGAAATTC	CCGGGTG	AGCCAC	CGCTCG	37
Query Match	6.0%	Score 28:	DB 21:	Length 184:		
Best Local Similarity	100.0%	Pred. No.	1.72e-26:			
Matches	28:	Conservative	0:	Mismatches	0:	Indels 0: Gaps 0:

BASE COUNT	47 a	66 c	25 t	17 others
ORIGIN				
Query Match	6.08;	Score 28;	DB 21;	Length 221;
Best Local Similarity	100.08;	Pred. No. 1.72e-26;		
Matches	28;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Db	25	GGAAATCCCGGGTCGACCCACGCGTCG 52		
Qy	29	ggaattcccggtcgacccacggtcgcg 56		
RESULT 12				
LOCUS	HSU46345	340 bp	EST	13-MAR-1997
DEFINITION	Human clone xs359 mRNA sequence.			
ACCESSION	U46345			
NID	91236487			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 340)			
AUTHORS	Gress,T.M., Muller-Pillasch,F., Geng,M., Zimmerhackl,F., Zehetner,G., Friess,H., Buchler,M., Adler,G. and Lehrach,H.			
TITLE	A pancreatic cancer-specific expression profile			
JOURNAL	Oncogene 13 (8), 1819-1830 (1996)			
MEDLINE	97050791			
REFERENCE	2 (bases 1 to 340)			
AUTHORS	Mueller-Pillasch,F., Zimmerhackl,F., Geng,M. and Gress,T.M.			
TITLE	Direct Submission			
JOURNAL	Submitted (16-JAN-1996) Internal Medicine I, University of Ulm, Robert-Koch-Strasse 8, Ulm, Baden-Wuerttemberg 89081, Germany			
FEATURES	Location/Qualifiers			
source	1..340			
	/organism="Homo sapiens"			
	/note="overexpressed in pancreatic cancer"			
	/db_xref="taxon:9606"			
	/cell_line="Patu 8988t"			
	/tissue_type="pancreatic cancer"			
	/clone="xs359"			
BASE COUNT	78 a	79 c	64 g	95 t 24 others
ORIGIN				
Query Match	6.08;	Score 28;	DB 23;	Length 340;
Best Local Similarity	100.08;	Pred. No. 1.72e-26;		
Matches	28;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
Db	31	GGAAATCCCGGGTCGACCCACGCGTCG 58		
Qy	29	ggaattcccggtcgacccacggtcgcg 56		
RESULT 13				
LOCUS	HSU46346	350 bp	EST	13-MAR-1997
DEFINITION	Human clone xs360 mRNA sequence.			
ACCESSION	U46346			
NID	91236488			
KEYWORDS	EST.			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 350)			
AUTHORS	Gress,T.M., Muller-Pillasch,F., Geng,M., Zimmerhackl,F., Zehetner,G., Friess,H., Buchler,M., Adler,G. and Lehrach,H.			
TITLE	A pancreatic cancer-specific expression profile			
JOURNAL	Oncogene 13 (8), 1819-1830 (1996)			
MEDLINE	97050791			
REFERENCE	2 (bases 1 to 350)			
AUTHORS	Mueller-Pillasch,F., Zimmerhackl,F., Geng,M. and Gress,T.M.			
TITLE	Direct Submission			

JOURNAL Submitted (16-JAN-1996) Internal Medicine I, University of Ulm,  
Robert-Koch-Strasse 8, Ulm, Baden-Wuerttemberg 89081, Germany

FEATURES  
Source  
Location/Qualifiers  
1..350  
/organism="Homo sapiens"  
/note="overexpressed in pancreatic cancer"  
/db\_xref="taxon:9606"  
/cell\_line="Patu 8988t"  
/tissue\_type="pancreatic cancer"  
/clone="xs360"

BASE COUNT 104 a 59 c 77 g 99 t 11 others  
ORIGIN

Query Match 6.0%; Score 28; DB 23; Length 350;  
Best Local Similarity 100.0%; Pred. No. 1.72e-26;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 34 GGAATTCGGGTGACCCACGCGTCGC 61  
|||||  
Qy 29 ggaattccgggtgacccacgcggtccg 56

RESULT 14  
LOCUS HSU46350 360 bp mRNA EST 13-MAR-1997  
DEFINITION Human clone xs366 mRNA sequence.  
ACCESSION U46350  
NID q1236492  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 360)  
Gress.T.M., Muller-Pillasch,F., Geng,M., Zimmerhackl,F.,  
Zenetner,G., Friess,H., Buchler,M., Adler,G. and Lehrach,H.  
A pancreatic cancer-specific expression profile  
Oncogene 13 (8), 1819-1830 (1996)  
97050791  
2 (bases 1 to 360)  
Muller-Pillasch,F., Zimmerhackl,F., Geng,M. and Gress,T.M.  
Direct Submission  
Submitted (16-JAN-1996) Internal Medicine I, University of Ulm,  
Robert-Koch-Strasse 8, Ulm, Baden-Wuerttemberg 89081, Germany

FEATURES  
Source  
Location/Qualifiers  
1..360  
/organism="Homo sapiens"  
/note="overexpressed in pancreatic cancer"  
/db\_xref="taxon:9606"  
/cell\_line="Patu 8988t"  
/tissue\_type="pancreatic cancer"  
/clone="xs366"

BASE COUNT 53 a 95 c 129 g 67 t 16 others  
ORIGIN

Query Match 6.0%; Score 28; DB 23; Length 360;  
Best Local Similarity 100.0%; Pred. No. 1.72e-26;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 40 GGAATTCGGGTGACCCACGCGTCGC 67  
|||||  
Qy 29 ggaattccgggtgacccacgcggtccg 56

RESULT 15  
LOCUS T18713 386 bp mRNA EST 17-OCT-1996  
DEFINITION 5C04G09-T7 membrane-free polysomes from endosperm Zea mays cDNA  
clone 5C04G09 5' end similar to 40s ribosomal protein S8, mRNA  
sequence.  
ACCESSION T18713  
NID g485643  
KEYWORDS EST.  
SOURCE maize.  
ORGANISM Zea mays

Eukaryotes; mitochondrial eukaryotes; Viridiplantae;  
Charophyta;Embryophyta group; Embryophyta; Magnoliophyta;  
Liliopsida; Poales; Poaceae; Zea.  
1 (bases 1 to 386)  
Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T.,  
Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and  
Larkins,B.  
Partial sequencing and mapping of clones from two maize cDNA  
libraries  
Plant Mol. Biol. 26, 1085-1101 (1994)  
95111093

Contact: The Maize cDNA Project

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E-mail: robferl@nervm.nerdc.ufl.edu

Seq primer: T7.  
Location/Qualifiers  
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/organism="Zea mays"  
/strain="W64A2"  
/note="Vector: zipLox; Site\_1: SalI; Site\_2: NotI; ds-cDNA  
was prepared from oligo-dt selected mRNA by priming with a  
NotI oligo- dt oligomer and then adding the second strand  
to RNase-nicked DNA:RNA hybrid with DNA POLI. SalI  
adaptors were added to the ends, the ds-cDNAs were then  
digested with NotI and size-selected. These were  
directionally-cloned into the zipLox phage vector, excised  
as plasmids, and then individually analyzed."  
/db\_xref="taxon:4577"  
/clone="5C04G09"  
/clone\_lib="membrane-free polysomes from endosperm"  
/lab\_host="DH10B"  
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FEATURES  
Source  
Location/Qualifiers  
1..386  
/organism="Zea mays"  
/strain="W64A2"  
/note="Vector: zipLox; Site\_1: SalI; Site\_2: NotI; ds-cDNA  
was prepared from oligo-dt selected mRNA by priming with a  
NotI oligo- dt oligomer and then adding the second strand  
to RNase-nicked DNA:RNA hybrid with DNA POLI. SalI  
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digested with NotI and size-selected. These were  
directionally-cloned into the zipLox phage vector, excised  
as plasmids, and then individually analyzed."  
/db\_xref="taxon:4577"  
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/clone\_lib="membrane-free polysomes from endosperm"  
/lab\_host="DH10B"  
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Best Local Similarity 100.0%; Pred. No. 1.72e-26;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 25 GGAATTCGGGTGACCCACGCGTCGC 52  
|||||  
Qy 29 ggaattccgggtgacccacgcggtccg 56

Search completed: Mon Mar 8 23:35:10 1999

Job time : 1491 secs.

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\*\*\*\*\*  
M P S R L H  
\*\*\*\*\* (TM)  
\*\*\*\*\*

Release 3.1A John F. Collins, Biocomputing Research Unit.  
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MPSrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Mon Mar 8 22:14:44 1999; MasPar time 35.64 Seconds  
Tabular output not generated.  
1138.185 Million cell updates/sec

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Description: (1-469) from US09206040A.seq  
Perfect Score: 465  
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Comp: aattgaacgcgcnggtcca.....ctactatgaactctanna

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 165359 seqs, 43243793 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: n-issued  
1:5A\_COMB 2:5B\_COMB 3:5C\_COMB 4:PCT9\_COMB 5:backfiles1

Statistics: Mean 7.884; Variance 3.978; scale 1.982

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
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2	40	8.6	1023	3	US-08-785-Sequence 2, Applicati	1.91e-13	
3	38	8.2	570	3	US-08-633-Sequence 1, Applicati	4.81e-12	
4	38	8.2	969	3	US-08-700-Sequence 1, Applicati	4.81e-12	
5	38	8.2	1529	3	US-08-726-Sequence 1, Applicati	4.81e-12	
6	38	8.2	1581	3	US-08-460-Sequence 1, Applicati	4.81e-12	
7	38	8.2	1581	2	US-08-383-Sequence 1, Applicati	4.81e-12	
8	37	8.0	965	3	US-08-388-Sequence 22, Applicati	2.38e-11	
9	36	7.7	7218	2	US-08-232-Sequence 14, Applicati	1.16e-10	
10	29	6.2	215	1	US-08-238-Sequence 5, Applicati	5.54e-06	
11	27	5.8	215	1	US-08-238-Sequence 5, Applicati	1.05e-04	
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13	27	5.8	2606	3	US-08-568-Sequence 22, Applicati	1.05e-04	
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c	30	21	4.5	65	1	US-08-471-Sequence 145, Applicat	4.31e-01	
c	31	21	4.5	66	1	US-08-471-Sequence 144, Applicat	4.31e-01	
c	32	21	4.5	68	1	US-08-471-Sequence 143, Applicat	4.31e-01	
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ALIGNMENTS

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AC xxxxxx  
DT  
DE Sequence 14, Application US/08232463  
CC Sequence 14, Application US/08232463  
CC Patent No. 5670367  
CC GENERAL INFORMATION:  
CC APPLICANT: DORNER, F.  
CC APPLICANT: SCHEIFLINGER, F.  
CC APPLICANT: FALKNER, F. G.  
CC TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
CC NUMBER OF SEQUENCES: 52  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Foley & Lardner  
CC STREET: 1800 Diagonal Road, Suite 500  
CC CITY: Alexandria  
CC STATE: VA  
CC COUNTRY: USA  
CC ZIP: 22313-0299  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: Patent In Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/232,463  
CC FILING DATE:  
CC CLASSIFICATION: 435  
CC PRIOR APPLICATION DATA:  
CC APPLICATION NUMBER: US/07/935,313  
CC FILING DATE:  
CC APPLICATION NUMBER: EP 91 114 300.6  
CC FILING DATE: 26-AUG-1991  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: BENT, Stephen A.  
CC REGISTRATION NUMBER: 29,768  
CC REFERENCE/DOCKET NUMBER: 30472/114 IMMU  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (703)836-9300  
CC TELEFAX: (703)683-4109  
CC TELEX: 899149  
CC INFORMATION FOR SEQ ID NO: 14:  
CC SEQUENCE CHARACTERISTICS:

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CC LENGTH: 7218 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC IMMEDIATE SOURCE:
CC TOPOLOGY: linear
CC LIBRARY: Consensus
CC CLONE: Consensus
CC CLONE: PTZgpt-Fls
SQ SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.

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Best Local Similarity 0.5%; Pred. No. 5.20e-17;
Matches 1; Conservative 127; Mismatches 83; Indels 0; Gaps 0;

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Db 1405 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1435
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ID US-08-785-065-2 STANDARD; DNA; UNC; 1023 BP.
CC xxxxxx
DT
DE Sequence 2, Application US/08785065
DE Sequence 2, Application US/08785065
CC Patent No. 5814451
CC GENERAL INFORMATION:
CC APPLICANT: Bandman, Olga
CC APPLICANT: Goli, Surya K.
CC APPLICANT: Hillman, Jennifer L.
CC TITLE OF INVENTION: NOVEL SUBUNITS OF NADH DEHYDROGENASE
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Incyte Pharmaceuticals, Inc.
CC STREET: 3174 Porter Drive
CC CITY: Palo Alto
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq for Windows Version 2.0
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CC APPLICATION NUMBER: US/08/785,065
CC FILING DATE: Herewith
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER:
CC FILING DATE:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Billings, Lucy J.
CC REGISTRATION NUMBER: 36,749
CC REFERENCE/DOCKET NUMBER: PF-0187 US
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-855-0555
CC TELEFAX: 415-845-4166
CC TELEX:
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 1023 base pairs
CC TYPE: nucleic acid
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AC xxxxxx
DE Sequence 1, Application US/08700637
DE Sequence 1, Application US/08700637
CC Patent No. 5854413
CC GENERAL INFORMATION:
CC APPLICANT: Hawkins, Phillip R.
CC APPLICANT: Stuart, Susan G.
CC APPLICANT: Murry, Lynn E.
CC TITLE OF INVENTION: NOVEL SYNAPTOGYRIN HOMOLOG FROM COLON
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Incyte Pharmaceuticals, Inc.
CC STREET: 3174 Porter Drive
CC CITY: Palo Alto
CC STATE: CA
CC COUNTRY: U.S.
CC ZIP: 94304
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette
CC COMPUTER: IBM Compatible
CC OPERATING SYSTEM: DOS
CC SOFTWARE: FastSeq Version 1.5
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08700,637
CC FILING DATE: Filed Herewith
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Luther, Barbara J.
CC REGISTRATION NUMBER: 33,954
CC REFERENCE/DOCKET NUMBER: PF-0065 US
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-855-0555
CC TELEFAX: 415-852-0195
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 969 base pairs
CC TYPE: nucleic acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: cDNA
CC IMMEDIATE SOURCE:
CC LIBRARY: COLNOT05
CC CLONE: 775426
CC SEQUENCE 969 BP; 163 A; 324 C; 280 G; 202 T; 0 OTHER.

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Best Local Similarity 95.1%; Pred. No. 4.81e-12;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 16 cagggtancggtcagggaattcccggtcgcacccacgcgctccg 56

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ID US-08-726-575A-1 STANDARD; DNA; UNC; 1529 BP.
AC xxxxxx
DE Sequence 1, Application US/08726575A
DE Sequence 1, Application US/08726575A
CC Patent No. 5834587
CC GENERAL INFORMATION:
CC APPLICANT: Winnie Chan, Derk J. Bergsma,
CC APPLICANT: Catherine E. Ellis
CC TITLE OF INVENTION: A No. 5834587el G-Protein Coupled Receptor,
CC TITLE OF INVENTION: HLTEX11
CC NUMBER OF SEQUENCES: 5
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: SmithKline Beecham Corporation
CC STREET: 709 Swedeland Road, P.O. Box 1539
CC CITY: King of Prussia
CC STATE: PA

Query Match 8.2%; Score 38; DB 3; Length 969;
Best Local Similarity 95.1%; Pred. No. 4.81e-12;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 46 CAGGTACCGTCCGGAATTCGCGGTGCGACCCACGCGTCCG 86
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RESULT 6
ID US-08-460-898-1 STANDARD; DNA; UNC; 1581 BP.
AC xxxxxx
DE Sequence 1, Application US/08460898
DE Sequence 1, Application US/08460898
CC Patent No. 5850022
CC GENERAL INFORMATION:
CC APPLICANT: Dehesh, Katayoon
CC APPLICANT: Voelker, Toni Alois
CC APPLICANT: Hawkins, Deborah
CC APPLICANT: Davies, Huw Maelor
CC TITLE OF INVENTION: Production of Myristate in Plant Cells
CC NUMBER OF SEQUENCES: 17
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Calgene, Inc.
CC STREET: 1920 Fifth Street
CC CITY: Davis
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 95616
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Diskette, 3.50 inch, 2.0 MB
CC COMPUTER: Apple Macintosh
CC OPERATING SYSTEM: Macintosh 7.0
CC SOFTWARE: Microsoft Word 5.1(a)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/460,898
CC FILING DATE: 05-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/383,756
CC FILING DATE: 02-FEB-1995
CC CLASSIFICATION: 435
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CC REFERENCE/DOCKET NUMBER: LUD 5409  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 212-688-9200  
CC TELEFAX: 212-838-3884  
CC INFORMATION FOR SEQ ID NO: 22:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 965 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: unknown  
CC TOPOLOGY: unknown  
CC MOLECULE TYPE: DNA (genomic)  
CC SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.

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Best Local Similarity 19.3%; Pred. No. 2.38e-11;

Matches 21; Conservative 53; Mismatches 34; Indels 1; Gaps 1;

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Cp 383 cctcgtcgtctccacagccttccacgcgtagtagaa-gcgaagtggaacatgg 325

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Cp 324 agatgaggagcgcggaatgcggatcattattgccctactcggagag 276

RESULT 9

ID US-08-232-463-14 STANDARD; DNA; UNC; 7218 BP.

AC xxxxxx

DT

DE Sequence 14, Application US/08232463

CC Sequence 14, Application US/08232463

CC Patent No. 5670367

CC GENERAL INFORMATION:

CC APPLICANT: DORNER, F.

CC APPLICANT: SCHEIFLINGER, F.

CC APPLICANT: FALKNER, F. G.

CC TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

CC NUMBER OF SEQUENCES: 52

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Foley & Lardner

CC STREET: 1800 Diagonal Road, Suite 500

CC CITY: Alexandria

CC STATE: VA

CC COUNTRY: USA

CC ZIP: 22313-0299

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/232,463

CC FILING DATE:

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US/07/935,313

CC FILING DATE:

CC APPLICATION NUMBER: EP 91 114 300.6

CC FILING DATE: 26-AUG-1991

CC ATTORNEY/AGENT INFORMATION:

CC NAME: BENT, Stephen A.

CC REGISTRATION NUMBER: 29,768

CC REFERENCE/DOCKET NUMBER: 30472/114 IMMU

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (703)836-9300

CC TELEFAX: (703)683-4109

CC TELEX: 899149

CC INFORMATION FOR SEQ ID NO: 14:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 7218 base pairs

CC TYPE: nucleic acid

CC STRANDEDNESS: single

CC

CC TOPOLOGY: linear  
CC IMMEDIATE SOURCE:  
CC CLONE: PTZgpt-Fls  
CC SEQUENCE 7218 BP; 1944 A; 1491 C; 1486 G; 1929 T; 368 OTHER.

Query Match 7.7%; Score 36; DB 2; Length 7218;

Best Local Similarity 4.3%; Pred. No. 1.16e-10;

Matches 4; Conservative 61; Mismatches 29; Indels 0; Gaps 0;

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Cp 89 tcccccccttctgtcgttcttcttcttcttcttcttcttcttcttcttcttctt 56

RESULT 10

ID US-08-238-163-5 STANDARD; DNA; UNC; 215 BP.

AC xxxxxx

DE

CC Sequence 5, Application US/08238163

CC Sequence 5, Application US/08238163

CC Patent No. 5369830

CC GENERAL INFORMATION:

CC APPLICANT: BENNETT, Alan

CC APPLICANT: LABAVITCH, John M.

CC APPLICANT: POWELL, Ann

CC APPLICANT: STOTZ, Henrik

CC TITLE OF INVENTION: PLANT INHIBITORS OF FUNGAL

CC TITLE OF INVENTION: POLYGALACTURONASES AND THEIR USE TO CONTROL FUNGAL DISEA

CC NUMBER OF SEQUENCES: 24

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Townsend and Townsend Khourie and Crew

CC STREET: Steuart Street Tower, One Market Plaza

CC CITY: San Francisco

CC STATE: California

CC COUNTRY: US

CC ZIP: 94105-1493

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/238,163

CC FILING DATE: 03-MAY-1994

CC CLASSIFICATION: 800

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Bastian, Kevin L.

CC REGISTRATION NUMBER: 34,774

CC REFERENCE/DOCKET NUMBER: 2307E-540

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 543-9600

CC TELEFAX: (415) 543-5043

CC INFORMATION FOR SEQ ID NO: 5:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 215 base pairs

CC TYPE: nucleic acid

CC STRANDEDNESS: single

CC TOPOLOGY: unknown

CC MOLECULE TYPE: protein

CC FEATURE:

CC NAME/KEY: misc\_feature

CC LOCATION: 1..215

CC OTHER INFORMATION: /standard\_name="Deduced amino acid

CC OTHER INFORMATION: sequence of PGIP from bean."

CC SEQUENCE 215 BP; 15 A; 8 C; 25 G; 26 T; 141 OTHER.

CC

Query Match

Best Local Similarity 6.2%; Score 29; DB 1; Length 215;

Matches 19; Conservative 65; Mismatches 67; Indels 1; Gaps 1;



RESULT 13  
ID US-08-568-459A-7 STANDARD; DNA; UNC; 2606 BP.  
AC xxxxxx  
DE Sequence 7, Application US/08568459A  
DE Sequence 7, Application US/08568459A  
CC Patent No. 5849306  
CC GENERAL INFORMATION:  
CC APPLICANT: Slim, Kim L.  
CC APPLICANT: Chitnis, Chetan  
CC APPLICANT: Miller, Louis H.  
CC APPLICANT: Peterson, David S.  
CC APPLICANT: Su, Xin-zhaun  
CC APPLICANT: Wellens, Thomas E.  
CC TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX  
CC TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS  
CC NUMBER OF SEQUENCES: 37  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Knobe Martens Olson & Bear  
CC STREET: 620 Newport Center Drive 16th Floor  
CC CITY: Newport Beach  
CC STATE: California  
CC COUNTRY: US  
CC ZIP: 92660  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.25  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/568,459A  
CC FILING DATE: 07-DEC-1995  
CC CLASSIFICATION: 435  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Israelisen, Ned  
CC REGISTRATION NUMBER: 29,955  
CC REFERENCE/DOCKET NUMBER: NIH121.001CP1  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: (619) 235-8550  
CC TELEFAX: (619) 235-0176  
CC INFORMATION FOR SEQ ID NO: 7:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 2606 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: single  
CC TOPOLOGY: linear  
CC MOLECULE TYPE: DNA (genomic)  
CC HYPOTHETICAL: NO  
CC ORIGINAL SOURCE:  
CC ORGANISM: Plasmodium falciparum  
CC SEQUENCE 2606 BP; 992 A; 351 C; 569 G; 694 T; 0 OTHER.  
Query Match 5.8%; Score 27; DB 3; Length 2606;  
Best Local Similarity 93.3%; Pred. No. 1.05e-04;  
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Db 42 CAGGTACCGGTCGGGAATCCCGGGTCGAC 71  
QY 16 caggtagcgtcagggaattcccggtcgac 45  
RESULT 14  
ID US-08-388-672A-22 STANDARD; DNA; UNC; 965 BP.  
AC xxxxxx  
DE Sequence 22, Application US/08388672A  
DE Sequence 22, Application US/08388672A  
CC Patent No. 5795961  
CC GENERAL INFORMATION:  
CC APPLICANT: Wallace, T. Paul  
CC APPLICANT: Harris, William J.  
CC APPLICANT: Carr, Frank J.

CC APPLICANT: Old, Lloyd J.  
CC APPLICANT: Welt, Sydney  
CC APPLICANT: Kitamura, Kunio  
CC TITLE OF INVENTION: Recombinant Human Anti-Lewis B  
CC TITLE OF INVENTION: Antibodies  
CC NUMBER OF SEQUENCES: 25  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Felfe and Lynch  
CC STREET: 805 Third Avenue  
CC CITY: New York  
CC STATE: New York  
CC COUNTRY: U.S.A.  
CC ZIP: 10022  
CC COMPUTER READABLE FORM:  
CC MEDIUM TYPE: Floppy disk  
CC COMPUTER: IBM PC compatible  
CC OPERATING SYSTEM: PC-DOS/MS-DOS  
CC SOFTWARE: PatentIn Release #1.0, Version #1.30  
CC CURRENT APPLICATION DATA:  
CC APPLICATION NUMBER: US/08/388,672A  
CC FILING DATE: 14-FEB-1995  
CC CLASSIFICATION:  
CC ATTORNEY/AGENT INFORMATION:  
CC NAME: Hanson, No. 5795961man D.  
CC REGISTRATION NUMBER: 30,946  
CC REFERENCE/DOCKET NUMBER: LUD 5409  
CC TELECOMMUNICATION INFORMATION:  
CC TELEPHONE: 212-688-9200  
CC TELEFAX: 212-838-3884  
CC INFORMATION FOR SEQ ID NO: 22:  
CC SEQUENCE CHARACTERISTICS:  
CC LENGTH: 965 base pairs  
CC TYPE: nucleic acid  
CC STRANDEDNESS: unknown  
CC TOPOLOGY: unknown  
CC MOLECULE TYPE: DNA (genomic)  
CC SEQUENCE 965 BP; 192 A; 170 C; 226 G; 200 T; 177 OTHER.  
Query Match 5.6%; Score 26; DB 3; Length 965;  
Best Local Similarity 15.8%; Pred. No. 4.45e-04;  
Matches 22; Conservative 60; Mismatches 56; Indels 1; Gaps 1;  
Db 810 WYRGWGVDYGGGYNYNGKRGVMTADTSSNSRSVTAADTAVYCVGRSYDSGDGY 869  
QY 256 tcaggggatcgatcgacagactctccagatggcaataatcgatcccgattccgcgc 315  
Db 870 WGGTIVTVSSHUVKMTSSSSASVGDRTVTCRSSSTTHGNTYNYWYKRAKRVNSRSGV 929  
QY 316 tctcatctcc-atgttcgaccttcgtttctctatctacgtcgctggaaggtgtgagcag 374  
Db 930 SRSGSGGTDYTTSSDATY 948  
QY 375 gacgcagagaatcgcggtt 393  
RESULT 15  
ID PCT-US95-11934-94 STANDARD; DNA; UNC; 74 BP.  
AC xxxxxx  
DE Sequence 94, Application PC/TUS9511934  
DE Sequence 94, Application PC/TUS9511934  
CC GENERAL INFORMATION:  
CC APPLICANT: Cytogen Corporation  
CC TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From  
CC TITLE OF INVENTION: Peptide Libraries  
CC NUMBER OF SEQUENCES: 103  
CC CORRESPONDENCE ADDRESS:  
CC ADDRESSEE: Pennie & Edmonds  
CC STREET: 1155 Avenue of the Americas  
CC CITY: New York  
CC STATE: New York  
CC COUNTRY: USA  
CC ZIP: 10036





\*\*\*\*\*

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 21:44:20 1999; MasPar time 628.63 Seconds  
Tabular output not generated.  
1336.036 Million cell updates/sec

Title: >US-09-206-040-1  
Description: (1-469) from US09206040A.seq  
Perfect Score: 465  
N.A. Sequence: 1 ttaactgcagcgcgcaggt.....gatgatcatcattgaagatnnt 469  
Comp: aattgaacgtcgcnggtcca.....ctactatgaactctctanna

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 2275026 seqs, 895388244 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: emb1-est56

Database: 1:em\_est1 2:em\_gss1 3:em\_gss2 4:em\_gss3

5:gb\_est1 6:gb\_est10 7:gb\_est11 8:gb\_est12 9:gb\_est13  
10:gb\_est14 11:gb\_est15 12:gb\_est16 13:gb\_est17  
14:gb\_est18 15:gb\_est19 16:gb\_est20 17:gb\_est21  
18:gb\_est22 19:gb\_est23 20:gb\_est24 21:gb\_est25 22:gb\_est26  
23:gb\_est27 24:gb\_est28 25:gb\_est29 26:gb\_gss1 27:gb\_gss2  
28:gb\_gss3 29:gb\_gss4

Statistics: Mean 10.263; Variance 1.889; scale 5.433

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	81	17.4	462	9	C74877 Rice cDNA, partial seq 4.58e-113	
2	62	13.3	252	12	AA754459 97SN1787 Rice Immature 1.43e-74	
3	52	11.2	252	12	AA754459 97SN1787 Rice Immature 1.86e-55	
4	48	10.3	247	12	AA754458 97SN1784 Rice Immature 1.35e-47	
5	45	9.7	247	12	AA754458 97SN1784 Rice Immature 4.80e-42	
6	40	8.6	468	21	T18678 5C04C06-t7 membrane-fr 4.95e-33	
7	40	8.6	568	21	T18698 5C04F08-t7 membrane-fr 4.95e-33	
8	39	8.4	390	23	HSU46351 Human clone xs366 mRNA 2.86e-31	
9	39	8.4	436	21	T18686 5C04E09-t7 membrane-fr 2.86e-31	
10	39	8.4	583	21	T14703 5C04A02-t7 membrane-f 2.86e-31	
11	39	8.4	589	9	HS299396 Homo sapiens mRNA; exp 2.86e-31	
12	39	8.4	669	21	T18686 5C02H01-t7 membrane-fr 2.86e-31	
13	38	8.2	163	21	T18683 5C04E02-t7 membrane-fr 1.59e-29	

14	38	8.2	360	23	HSU46350 Human clone xs366 mRNA 1.59e-29
15	38	8.2	364	21	T14653 05C03g08-f21 membrane- 1.59e-29
16	38	8.2	370	23	HSU46347 Human clone xs361 mRNA 1.59e-29
17	38	8.2	373	21	T18695 5C04F05-t7 membrane-fr 1.59e-29
18	38	8.2	376	21	T18677 5C04B01-t7 membrane-fr 1.59e-29
19	38	8.2	379	21	T14744 05C04h07-f21 membrane- 1.59e-29
20	38	8.2	392	21	T18721 5C04H03-t7 membrane-fr 1.59e-29
21	38	8.2	400	23	HSU46349 Human clone xs363 mRNA 1.59e-29
22	38	8.2	404	21	T18665 5C02G02-t7 membrane-fr 1.59e-29
23	38	8.2	414	21	T18701 5C04G01-t7 membrane-fr 1.59e-29
24	38	8.2	414	21	T18700 5C04F10-t7 membrane-fr 1.59e-29
25	38	8.2	416	21	T18706 5C04G04-t7 membrane-fr 1.59e-29
26	38	8.2	430	23	HSU46341 Human clone xs353 mRNA 1.59e-29
27	38	8.2	431	21	T18292 5C06C07-t7 membrane-fr 1.59e-29
28	38	8.2	432	21	T18675 5C04A03-t7 membrane-fr 1.59e-29
29	38	8.2	432	21	T18703 5C04G02-t7 membrane-fr 1.59e-29
30	38	8.2	432	21	T18723 5C04H05-t7 membrane-fr 1.59e-29
31	38	8.2	436	21	T18699 5C04F09-t7 membrane-fr 1.59e-29
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34	38	8.2	450	21	T18285 5C06B04-t7 membrane-fr 1.59e-29
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37	38	8.2	458	21	T18684 5C04E07-t7 membrane-fr 1.59e-29
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41	38	8.2	579	18	AI142137 GDM00L51 human embryo 1.59e-29
42	38	8.2	744	23	AA220873 13 Pinus radiata post 1.59e-29
43	38	8.2	815	18	AI142131 GDM00L19 human embryo 1.59e-29
44	38	8.2	881	18	AI142132 GDM00L03 human embryo 1.59e-29
45	38	8.2	895	18	AI142134 GDM00L05 human embryo 1.59e-29

## ALIGNMENTS

RESULT 1 C74877 462 bp mRNA EST 18-SEP-1997  
LOCUS Rice cDNA, partial sequence (E60595\_1A), mRNA sequence.  
DEFINITION C74877  
ACCESSION  
NID 92443106  
KEYWORDS EST; EST(expressed sequence tag).  
SOURCE Oryza sativa (strain:Nipponbare) immature leaf including apical meristem (under short day condition) cDNA to mRNA.

ORGANISM Oryza sativa  
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;  
Embryophyta; vascular plants; seed plants; Magnoliophyta;  
Liliopsida; Poales; Poaceae; Oryza.  
REFERENCE 1 (sites)  
AUTHORS Sasaki,T. and Yamamoto,K.  
TITLE Rice cDNA from immature leaf including apical meristem  
JOURNAL Unpublished (1997)  
REFERENCE 2 (bases 1 to 462)  
AUTHORS Sasaki,T.  
TITLE Direct Submission  
JOURNAL Submitted (13-AUG-1997) to the DDBJ/EMBL/GenBank databases. Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba Ibaraki 305, Japan (E-mail:tsasaki@affrc.go.jp, Tel:0298-38-7441, Fax:0298-38-7468)  
PROJECT "RGP".

COMMENT Location/Qualifiers  
FEATURES  
source  
1. 462  
/organism="Oryza sativa"  
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/db\_xref="taxon:4530"  
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BASE COUNT 117 a 103 c 145 g 93 t 4 others

Query Match 17.4%; Score 81; DB 9; Length 462;

Best Local Similarity 72.9%; Pred. No. 4.58e-113;



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RESULT 4
LOCUS AA754458 247 bp mRNA EST 20-JAN-1998
DEFINITION 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
ACCESSION AA754458
NID 92801164
KEYWORDS EST.
SOURCE rice.
ORGANISM Oryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
1 (bases 1 to 247)
REFERENCE
AUTHORS Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL Unpublished (1998)
COMMENT
Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0301
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhna@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
FEATURES
Location/Qualifiers
1..247
/organism="Oryza sativa"
/cultivar="Milyang23"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
/clone="97SN1784"
/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
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ORIGIN
Query Match 10.3%; Score 48; DB 12; Length 247;
Best Local Similarity 14.6%; Pred. No. 1.35e-47;
Matches 31; Conservative 103; Mismatches 73; Indels 5; Gaps 5;
Db 17 BAWNKHHTMMTBWCCVRRVGTITNNGKHNG-RTTWNDCSDNAHCRTVVBWYARSKY 75
QY 203 caatacataatcgtcataagaatgcattgcattgattcattcaaatgcagatcagggg 262
Db 76 GYCTBYISWNVDTNTGGTGVGKTTVNVHSGWNNRCSNVVY-WBTAYCDYBYBDRANH 134
QY 263 atcgagtcacagactccagatggcaataatcgatccgcattccgcgctctcat 322
Db 135 VDTTRCTNRGICNYTASDNGTSATRVGTGDKTDSGCGGCKWKYV-YGSSBYBRCGVN 193
QY 323 ctccatgttcgccactt-tcg-cttctatctacgtcgctggaaggtgtggcaggacgca 380
Db 194 VMYRTTSMWTKSTKMBSDMSRRSRVHYGRW 225
QY 381 gagaatcgcgcttattctcatcaagaagcgtcga 412

RESULT 5
LOCUS AA754458 247 bp mRNA EST 20-JAN-1998
DEFINITION 97SN1784 Rice Immature Seed Lambda ZAPII cDNA Library Oryza sativa
ACCESSION AA754458
NID 92801164
KEYWORDS EST.
SOURCE rice.
ORGANISM Oryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
1 (bases 1 to 247)
REFERENCE
AUTHORS Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL Unpublished (1998)
COMMENT
Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0301
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhna@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
FEATURES
Location/Qualifiers
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/organism="Oryza sativa"
/cultivar="Milyang23"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
/db_xref="taxon:4530"
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/clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
BASE COUNT 7 a 16 c 21 g 34 t 169 others
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Best Local Similarity 11.4%; Pred. No. 4.80e-42;
Matches 24; Conservative 108; Mismatches 74; Indels 5; Gaps 5;
Db 19 WNNKHHTMMTBWCCVRRVGTITNNGKHNGRTTWNDCSDNAHCRTVVBWYARSKY 78
Cp 460 aatgtatcatccacagata-tagcagattgtccctcgccag-tgatctatcgagctct 403
Db 79 TBYISWNVDTNTGGTGVGKTTVNVHSGWNNRCSNVVYVWBTAYCDYBYBDRANHVD 138
Cp 402 tgatgagataaacgcgattctctgcgtctgcacagccttc-cagcgacgtagatagaa 344
Db 139 RCTNRDGCNYTA-SDNGT-SATKRVGTGDKTDSGCGGCKWKYVYGSBYBRCGVNV 196
Cp 343 gcgaagtgccgaatgagatgagatgagagcgcggaatcgcgagatcattattgccata 284
Db 197 RTTSMWTKSTKMBSDMSRRSRVHYGRWMB 227
Cp 283 ctggagagctgtgactcgatccctctgatct 253

RESULT 6
LOCUS T18678 468 bp mRNA EST 17-OCT-1996
DEFINITION 5C04C06-T7 membrane-free polysomes from endosperm Zea mays cDNA
clone 5C04C06 5' end similar to pyruvate phosphate dikinase, mRNA
sequence.
ACCESSION T18678
NID 9485608
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.

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KEYWORDS EST.
SOURCE rice.
ORGANISM Oryza sativa
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta; Liliopsida;
Poales; Poaceae; Oryza.
1 (bases 1 to 247)
REFERENCE
AUTHORS Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R., Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
TITLE Large-scale Sequencing Analysis of ESTs from Rice Immature Seed
JOURNAL Unpublished (1998)
COMMENT
Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0307
Fax: 82 331 290 0301
Email: myeun@sun20.asti.re.kr
Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhna@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
FEATURES
Location/Qualifiers
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/organism="Oryza sativa"
/cultivar="Milyang23"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site."
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BASE COUNT 7 a 16 c 21 g 34 t 169 others
ORIGIN
Query Match 9.7%; Score 45; DB 12; Length 247;
Best Local Similarity 11.4%; Pred. No. 4.80e-42;
Matches 24; Conservative 108; Mismatches 74; Indels 5; Gaps 5;
Db 19 WNNKHHTMMTBWCCVRRVGTITNNGKHNGRTTWNDCSDNAHCRTVVBWYARSKY 78
Cp 460 aatgtatcatccacagata-tagcagattgtccctcgccag-tgatctatcgagctct 403
Db 79 TBYISWNVDTNTGGTGVGKTTVNVHSGWNNRCSNVVYVWBTAYCDYBYBDRANHVD 138
Cp 402 tgatgagataaacgcgattctctgcgtctgcacagccttc-cagcgacgtagatagaa 344
Db 139 RCTNRDGCNYTA-SDNGT-SATKRVGTGDKTDSGCGGCKWKYVYGSBYBRCGVNV 196
Cp 343 gcgaagtgccgaatgagatgagatgagagcgcggaatcgcgagatcattattgccata 284
Db 197 RTTSMWTKSTKMBSDMSRRSRVHYGRWMB 227
Cp 283 ctggagagctgtgactcgatccctctgatct 253

RESULT 6
LOCUS T18678 468 bp mRNA EST 17-OCT-1996
DEFINITION 5C04C06-T7 membrane-free polysomes from endosperm Zea mays cDNA
clone 5C04C06 5' end similar to pyruvate phosphate dikinase, mRNA
sequence.
ACCESSION T18678
NID 9485608
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryotae; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.

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REFERENCE 1 (bases 1 to 468)  
 AUTHORS Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T., Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and Larkins,B.  
 TITLE Partial sequencing and mapping of clones from two maize cDNA libraries  
 JOURNAL Plant Mol. Biol. 26, 1085-1101 (1994)  
 MEDLINE 95111093  
 COMMENT Contact: The Maize cDNA Project

Helentjaris TG (primary contact)  
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 University of Arizona  
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 fax: 602-621-7186  
 E-mail: helnjars@cct.arizona.edu

Chris Baysdorfer  
 Department of Biological Sciences, School of Science  
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 Hayward, CA 94542  
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 fax: 510-727-2035  
 E-mail: cbaysdor@s1.csu Hayward.edu

Rob Ferl  
 Interdisciplinary Center for Biotechnology Research  
 DNA Sequencing Core  
 University of Florida  
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 Gainesville, FL 32611-0695  
 ph: 904-392-1928, ext. 301  
 fax: 904-392-4072  
 E-mail: robferl@nervm.nerdc.ufl.edu

Seq primer: T7.  
 Location/Qualifiers  
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 /strain="W64A2"  
 /note="Vector: ZipLox; Site\_1: SalI; Site\_2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo- dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA Pol. SalI adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."  
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 Query Match 8.6%; Score 40; DB 21; Length 468;  
 Best Local Similarity 89.6%; Pred. No. 4.95e-33;  
 Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Db 10 CAGGTACGGTCCGGAATCCCGGTGCACCCACGCGTCCGAGGCT 57  
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 Qy 16 caggtancggtcaggaaattccgcgggtgacccacgctccgtagcgct 63

RESULT 7  
 LOCUS T18698 568 bp mRNA EST 17-OCT-1996  
 DEFINITION 5C04F08-T7 membrane-free polysomes from endosperm Zea mays cDNA clone 5C04F08 5' end similar to 22kd alpha zein alpha precursor,

ACCESSION T18698  
 NID 9485628  
 KEYWORDS EST.  
 SOURCE maize.  
 ORGANISM Zea mays  
 Eukaryotae; mitochondrial eukaryotes; Viridiplantae; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.  
 REFERENCE 1 (bases 1 to 568)  
 AUTHORS Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T., Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and Larkins,B.  
 TITLE Partial sequencing and mapping of clones from two maize cDNA libraries  
 JOURNAL Plant Mol. Biol. 26, 1085-1101 (1994)  
 MEDLINE 95111093  
 COMMENT Contact: The Maize cDNA Project

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 fax: 904-392-4072  
 E-mail: robferl@nervm.nerdc.ufl.edu

Seq primer: T7.  
 Location/Qualifiers  
 1. 568  
 /organism="Zea mays"  
 /strain="W64A2"  
 /note="Vector: ZipLox; Site\_1: SalI; Site\_2: NotI; ds-cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo- dT oligomer and then adding the second strand to RNase-nicked DNA:RNA hybrid with DNA Pol. SalI adaptors were added to the ends, the ds-cDNAs were then digested with NotI and size-selected. These were directionally-cloned into the ZipLox phage vector, excised as plasmids, and then individually analyzed."  
 /db\_xref="taxon:4577"  
 /clone="5C04F08"  
 /clone\_lib="membrane-free polysomes from endosperm"  
 /lab\_host="DH10B"

BASE COUNT 153 a 183 c 104 g 123 t 5 others  
 Query Match 8.6%; Score 40; DB 21; Length 568;  
 Best Local Similarity 95.3%; Pred. No. 4.95e-33;  
 Matches 41; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Helentjaris TG (primary contact)  
Dept. of Plant Sciences

REFERENCE  
AUTHORS  
Shen, B., Carneiro, N., Torres-Jerez, I., Stevenson, R., McCreery, T., Helentjaris, T., Baysdorfer, C., Almira, E., Ferl, R., Habben, J., and Larkins, B.  
TITLE: Partial sequencing and mapping of clones from two maize cDNA libraries  
(bases 1 to 583)

```

JOURNAL      Plant Mol. Biol. 26, 1085-1101 (1994)
MEDLINE      95111093
COMMENT      Other ESTs: 05c04d02-f21
              Contact: The Maize cDNA Project

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ph: 904-392-1928, ext. 301
fax: 904-392-4072
E-mail: roberfer@nervm.nerdc.ufl.edu
Seq primer: T7.

FEATURES
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        Location/Qualifiers
            1..583
                /organism="Zea mays"
                /strain="W64A2"
                /note="Vector: ZipLox; Site_1: SalI; Site_2: NotI; ds-cDNA
                was prepared from oligo-dT selected mRNA by priming with a
                NotI oligo- dT oligomer and then adding the second strand
                to RNase-nicked DNA:RNA hybrid with DNA POLI. SalI
                adaptors were added to the ends, the ds-cDNAs were then
                digested with NotI and size-selected. These were
                directionally-cloned into the ZipLox phage vector, excised
                as plasmids, and then individually analyzed."
                /db_xref="taxon:4577"
                /clone="05c04d02"
                /clone_lib="membrane-free polysomes from endosperm"
                /lab_host="DH10B"
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BASE COUNT  155 a 104 c 175 g 146 t      3 others
ORIGIN
    mRNA
    CONTACT: The Maize cDNA Project

Query Match      8.4%; Score 39; DB 21; Length 583;
Best Local Similarity 88.0%; Pred. No. 2.86e-31;
Matches 44; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 12 CAGGTACCGGTCGGGAATTCGCGGGTCGACCCACGCGTCGGGGAGCTGC 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 16 caggtaacggtcagggaattcccggtcgaccacgcgctccgtacggctgc 65

RESULT 11
LOCUS      HS299396      589 bp      DNA      EST      19-SEP-1997
DEFINITION Homo sapiens mRNA; expressed sequence tag; clone DKFZphamyl_1c11,
3' read, mRNA sequence.
ACCESSION  Z99396
NID        g2415636
KEYWORDS   EST; expressed sequence tag.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
            Primates; Catarrhini; Homnidae; Homo.
REFERENCE  1 (bases 1 to 589)

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AUTHORS      Korn,B., Wiemann,S., Ebert,L. and Poustka,A.
JOURNAL      Unpublished
REFERENCE    2 (bases 1 to 589)
AUTHORS      Korn,B.
TITLE        Direct Submission
JOURNAL      Submitted (11-SEP-1997) Korn B., Institution Molekulare
              Genomanalyse, Deutsches Krebsforschungszentrum Heidelberg, Im
              Neuenheimer Feld 506, D-69120 Heidelberg, FRG
FEATURES
    source
        Location/Qualifiers
            1..589
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_lib="DKFZphamyl"
                /clone="DKFZphamyl_1c11"
                /tissue_type="amygdala"
                /dev_stage="adult"
BASE COUNT  161 a 156 c 151 g 120 t      1 others
ORIGIN
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    Best Local Similarity 95.2%; Pred. No. 2.86e-31;
    Matches 40; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 398 ACGGACGCGTGGTTCGACCGCGGAATTCGCGACCGGTACCTG 439
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Cp 57 acggacgctgggtcgaccgcgggaattcctgaccgntacctg 16

RESULT 12
LOCUS      T18668      669 bp      mRNA      EST      17-OCT-1996
DEFINITION 5C02H01-T7 membrane-free polysomes from endosperm Zea mays cDNA
clone 5C02H01 5' end, mRNA sequence.
ACCESSION  T18668
NID        9485598
KEYWORDS   EST.
SOURCE     Zea mays
            Eukaryota; Eukaryotes; Viridiplantae;
            Charophyta; Embryophyta group; Embryophyta; Magnoliophyta;
            Liliopsida; Poales; Poaceae; Zea.
REFERENCE  1 (bases 1 to 669)
AUTHORS      Shen,B., Carneiro,N., Torres-Jerez,I., Stevenson,R., McCreery,T.,
              Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and
              Larkins,B.
TITLE        Partial sequencing and mapping of clones from two maize cDNA
              libraries
JOURNAL      Plant Mol. Biol. 26, 1085-1101 (1994)
MEDLINE      95111093
COMMENT      Contact: The Maize cDNA Project

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```

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2. (bases 1 to 350)  
Mueller-Pillasch, F., Zimmerhackl, F., Geng, M. and Gress, T. M.  
Direct Submission  
TITLE  
Submitted (16-JAN-1996) Internal Medicine I, University of Ulm,  
JOURNAL  
Robert-Koch-Strasse 8, Ulm, Baden-Wuerttemberg 89081, Germany  
FEATURES  
Location/Qualifiers  
source  
1. 360  
/organism="Homo sapiens"  
/note="overexpressed in pancreatic cancer"

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/db_xref="taxon:9606"
/cell_line="Patu 8988t"
/tissue_type="pancreatic cancer"
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BASE COUNT      53 a      95 c      129 g      67 t      16 others
ORIGIN

Query Match      8.2%; Score 38; DB 23; Length 360;
Best Local Similarity 95.1%; Pred. No. 1.59e-29;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 27 CAGGTACCGTCCGGAATTCGCCGGTCCGACCCACGCGTCCG 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 16 caggtancggtcagggaattcccggtcgaccacgcgctccg 56

RESULT 15
LOCUS T14653 364 bp mRNA EST 17-OCT-1996
DEFINITION 05c03g08-f21 membrane-free polysomes from endosperm Zea mays cDNA
clone 05c03g08 3' end similar to starch branching enzyme II, mRNA
sequence.
ACCESSION T14653
NID 9440632
KEYWORDS EST.
SOURCE maize.
ORGANISM Zea mays
Eukaryotes; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
REFERENCE 1 (bases 1 to 364)
AUTHORS Shen,B., Carneiro,N., Torres-Verz,I., Stevenson,R., McCreery,T.,
Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and
Larkins,B.
TITLE Partial sequencing and mapping of clones from two maize cDNA
libraries
JOURNAL Plant Mol. Biol. 26, 1085-1101 (1994)
MEDLINE 95111093
COMMENT Other ESTs: 05c03g08-t7
Contact: The Maize cDNA Project

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Search completed: Mon Mar 8 22:09:57 1999  
Job time : 1537 secs.

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Query Match      8.2%; Score 38; DB 21; Length 364;
Best Local Similarity 95.1%; Pred. No. 1.59e-29;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 253 CGGACGCGTGGTCCGACCCCGGAATTCGGACCGGTACTCG 293
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Cp 56 cggacgcgtgggtcgaccccggaattcctgaccgntacctg 16

BASE COUNT      94 a      86 c      86 g      93 t      5 others
ORIGIN

Query Match      8.2%; Score 38; DB 21; Length 364;
Best Local Similarity 95.1%; Pred. No. 1.59e-29;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 253 CGGACGCGTGGTCCGACCCCGGAATTCGGACCGGTACTCG 293
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Job time : 1537 secs.

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/db_xref="taxon:9606"
/cell_line="Patu 8988t"
/tissue_type="pancreatic cancer"
/clone="xs366"

BASE COUNT      53 a      95 c      129 g      67 t      16 others
ORIGIN

Query Match      8.2%; Score 38; DB 23; Length 360;
Best Local Similarity 95.1%; Pred. No. 1.59e-29;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 27 CAGGTACCGTCCGGAATTCGCCGGTCCGACCCACGCGTCCG 67
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 16 caggtancggtcagggaattcccggtcgaccacgcgctccg 56

RESULT 15
LOCUS T14653 364 bp mRNA EST 17-OCT-1996
DEFINITION 05c03g08-f21 membrane-free polysomes from endosperm Zea mays cDNA
clone 05c03g08 3' end similar to starch branching enzyme II, mRNA
sequence.
ACCESSION T14653
NID 9440632
KEYWORDS EST.
SOURCE maize.
ORGANISM Zea mays
Eukaryotes; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; Magnoliophyta;
Liliopsida; Poales; Poaceae; Zea.
REFERENCE 1 (bases 1 to 364)
AUTHORS Shen,B., Carneiro,N., Torres-Verz,I., Stevenson,R., McCreery,T.,
Helentjaris,T., Baysdorfer,C., Almira,E., Ferl,R., Habben,J. and
Larkins,B.
TITLE Partial sequencing and mapping of clones from two maize cDNA
libraries
JOURNAL Plant Mol. Biol. 26, 1085-1101 (1994)
MEDLINE 95111093
COMMENT Other ESTs: 05c03g08-t7
Contact: The Maize cDNA Project

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Gainesville, FL 32611-0695
ph: 904-392-1928, ext. 301
fax: 904-392-4072
E-mail: roberferl@nrm.nerdc.ufl.edu
Seq primer: F21.
Location/Qualifiers
1..364
/organism="Zea mays"
/strain="W64A2"
/note="Vector: Ziplox; Site_1: SalI; Site_2: NotI; ds-cDNA
was prepared from oligo-dT selected mRNA by priming with a

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Result No.	Query			ID	Description	Pred. No.	
	Score	Match	Length				
c	1	39	8.4	204	1 N81164	Base substituted E.co	1.27e-10
	2	38	8.2	91	9 Q31746	Oligonucleotide probe	5.35e-10
	3	38	8.2	91	9 Q31746	Oligonucleotide probe	5.35e-10
c	4	38	8.2	570	37 T12175	cDNA encoding a novel	5.35e-10
	5	38	8.2	969	38 T96721	Human synaptogyrin cD	5.35e-10
	6	38	8.2	1581	22 T32233	Cuphea C14:0-ACP thio	5.35e-10
c	7	38	8.2	1698	40 V17199	Human MKK3-interactin	5.35e-10
	8	34	7.3	204	1 N81164	Base substituted E.co	1.52e-07
	9	32	6.9	114	12 Q70468	Generic DNA sequence	2.39e-06
c	10	30	6.5	114	12 Q70465	Generic DNA sequence	3.58e-05
	11	30	6.5	114	12 Q70467	Generic DNA sequence	3.58e-05
	12	30	6.5	114	12 Q70467	Generic DNA sequence	3.58e-05
c	13	29	6.2	114	12 Q70468	Generic DNA sequence	1.36e-04

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SQ      sequence      51 bp;      3 A;      17 C;      13 G;      4 T;
Query Match      8.2%;      Score 38;      DB 9;      Length 91;
Best Local Similarity 11.7%;      Pred. No. 5.35e-10;
Matches      7;      Conservative      42;      Mismatches 11;      Indels 0;      Gaps 0;

Db      2      gctccgcgcsvhsyyvvhvshhsvhhvhhvsvvvvhhvvhvhhvhyvsvvc 61
||| |||      :      :      :      :      :      :      :      :      :      :      :      :      :      :      :
Cp      141      gctgcggtgctactttctgctcaagaagtcaccaagaatccactctcttccccccc 82

RESULT      4

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AC	131273;	
DC	23-APR-1998	(first entry)
DE	cDNA encoding a novel beta-chemokine designated PTEC.	
KE	Beta-chemokine; PTEC; homologue; human RANTES; C-C Chemokine;	
DE	diagnosis; treatment; activated T cell;	
KW	immediate type hypersensitivity; leukocyte proliferation; ss.	
KW	homo sapiens.	
OS		
FH	Key	Location/Qualifiers
FT	CDS	110..391
FT		/*tag= a
PN	W09739126-A1.	
PD	23-OCT-1997.	
PF	14-APR-1997; U06249.	
PR	17-APR-1996; US-633682.	
PA	(INCY-) INCYTE PHARM INC.	
PI	Bandman O, Hawkins PR, Murry LE;	
DR	WPI; 97-526462/48.	
DR	P-PSDB; W21271.	
PT	PTEC, a novel human beta-chemokine - useful for diagnosing and	
PT	treating e.g. viral, bacterial, fungal infections, auto-immune	
PT	diseases, etc	
PS	Claim 2. Pages 39-40; 59pp; English.	
CC	The present DNA sequence encodes a novel beta-chemokine polypeptide	
CC	designated PTEC. The protein has Cys residues of a beta-chemokine (C32,	
CC	C33, C56 and C72). The present sequence was isolated from a cDNA library	
CC	generated from non-tumorous human prostate tissue. The PTEC protein is	

a homologue of human RANTES, which is a C-C chemokine with structural similarity to interleukin-8 and human MIP-1beta. The polynucleotide sequence encoding PTEC can be used to diagnose or treat a condition associated with the presence of activated T cells including viral, bacterial, fungal or helminthic infections, allergic or asthmatic responses, mechanical injury associated with trauma, arteriosclerosis, atherogenesis or collagen vascular diseases, autoimmune diseases such as rheumatoid arthritis, myasthenia gravis, systemic lupus erythematosus or haemolytic anaemia, leukaemia, lymphomas or carcinomas, and diseases of immediate type hypersensitivity which involve activation or excessive proliferation of leukocytes, particularly monocytes, macrophages, eosinophils, basophil, mast and T cells.

Sequence 570 BP: 149 A: 155 C: 138 G: 128 T;

CC	immediate type hypersensitivity which involve activation of excessive
CC	proliferation of leukocytes, particularly monocytes, macrophages,
CC	eosinophils, basophil, mast and T cells.
SC	Sequence 570 BP; 149 A; 155 C; 138 G; 128 T; 0;
	Query Match 8.2%; Score 38; DB 37; Length 570;
	Best Local Similarity 95.1%; Pred. NO. 5.35e-10;
	Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db	46 caggtaccggtccggattcccggggtcgaccacacgcgtccg 86
Qy	16 caggtancggtcagggaattcccggggtcgaccacacgcgtccg 56
RESULT	5
ID	T96721 standard; cDNA; 969 BP.
AC	T96721;
DT	27-APR-1998 (first entry)
DE	Human synaptogyrin cDNA
KW	Synaptogyrin; human; colon cancer; lung cancer; brain tumour;
KW	Crohn's disease; rheumatoid arthritis; AIDS; allergy; urticaria;
KW	juvenile diabetes; scleroderma; antitense; diagnosis; therapy; ss.
OS	Homo sapiens.
FT	Key
CDS	Location/Qualifiers
	110..784

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FT M09741143-AL. /*tag= a
PN 06-NOV-1997.
PD 30-APR-1997; U07378.
PR 30-APR-1996; US-700637.
PA (INCY- ) INCYTE PHARM INC.
PI Hawkins PR, Murry LE, Stuart SG:
DR WPI: 97-549677/50.
DR P-PSDB; W36516.
PT Novel human synaptogyrin homologue - useful for diagnosis and
PT treatment of, e.g. rheumatoid arthritis, Crohn's disease, cancers,
PT etc.
PS Claim 2; Page 46-47; 74pp; English.
CC This polynucleotide (snpg) identifies and encodes a novel human
CC synaptogyrin homologue (SNPG) (see W36516). It was initially
CC identified in Incyte Clone 775426 from a colon cDNA library
CC (COLN0705) prepared from a Crohn's disease patient. Also claimed
CC are: (1) an expression vector containing PN; (2) a host cell
CC transformed with the vector of (1); (3) the purified 224 amino acid
CC SNPG protein; (4) an antisense molecule complementary to PN; (5) an
CC antibody (Ab) specific for the polypeptide of (3); and (6) an
CC inhibitor specific for the polypeptide of (3). Human SNPG can be
CC used for the diagnosis and treatment of a disease associated with
CC synaptogyrin, especially Crohn's disease, rheumatoid arthritis,
CC asthma and cancers or tumours of the lung, colon or brain (claimed).
CC The antisense molecule, Ab or inhibitor can be used to treat, e.g.
CC AIDS, allergy, urticaria, juvenile diabetes, scleroderma, etc.
SQ Sequence 969 BP; 163 A; 324 C; 280 G; 202 T;

Query Match 8.2%; Score 38; DB 38; Length 969;
Best Local Similarity 95.1%; Pred. No. 5.35e-10;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 46 caggtaccggtccggaattcccggtgcaccacgcgctccg 86
QY 16 caggtancggtcagggaattcccggtgcaccacgcgctccg 56

RESULT 6
ID T32233 standard; cDNA: 1581 BP.
AC T32233;
DT 26-OCT-1996 (first entry)
DE Cuphea C14:0-ACP thioesterase cDNA clone MCR134 (CpRatB2).
KW Myristate; myristic acid; fatty acid; acyl-ACP thioesterase;
KW seed oil; oilseed; vegetable oil; Brassica; transgenic plant;
KW surfactant; ss.
OS Cuphea palustris.
FH Key Location/Qualifiers
FT cds 119..1354
FT /*tag= a
FT W09623892-A2.
PN 08-AUG-1996.
PD 01-FEB-1996; U01585.
PR 02-FEB-1995; US-383756.
PR 05-JUN-1995; US-460898.
PA (CALJ ) CALGENE INC.
PI Dehesh K, Hawkins D, Voelker TA;
DR WPI: 96-371439/37.
DR P-PSDB; W02081.
PT Recombinant prodn. of myristate in plant cells - using DNA with
PT preferential activity on C14 fatty acids from Cuphea palustris,
PT nutmeg and camphor, useful in detergent and food industries
PS Example 1: Fig 1A-1E; 77pp; English.
CC A cDNA clone (T32233), designated MCR134 (pCpRatB2), codes for Cuphea
CC palustris C14:0-ACP thioesterase (W02081), an enzyme that acts
CC primarily on C14:0-ACP substrates, forming C14:0 (myristate). It
CC was isolated from a developing seed cDNA library by screening with
CC sequences encoding medium-chain acyl-ACP thioesterases from Cuphea
CC hookeriana. Constructs for expression of clone MCR134 in plant seeds
CC under the control of napin or oleosin regulatory regions were prepd.
CC These allow high-level prodn. of myristate (useful in surfactants
CC and foods) in plant cells, e.g. Brassica.
SQ Sequence 1581 BP; 418 A; 356 C; 410 G; 397 T;

```

```

Query Match 8.2%; Score 38; DB 22; Length 1581;
Best Local Similarity 95.1%; Pred. No. 5.35e-10;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 41 caggtaccggtccggaattcccggtgcaccacgcgctccg 81
QY 16 caggtancggtcagggaattcccggtgcaccacgcgctccg 56

RESULT 7
ID V17199 standard; cDNA: 1698 BP.
AC V17199;
DT 10-JUN-1998 (first entry)
DE Human MKK3-interacting protein (MIP) encoding cDNA.
KW MKK3-interacting protein; MIP; mitogen activated protein kinase;
KW WAPK kinase-3; human; transduction; target; extracellular signal;
KW interfering mutant; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT cds 167..1213
FT /*tag= a
FT /product= "MKK3-interacting protein"
FT W09800339-A2.
PN 08-JAN-1998.
PD 02-JUL-1997; U10866.
PR 01-JUL-1997; US-886572.
PR 03-JUL-1996; US-021224.
PR 12-JUL-1996; US-021641.
PA (CHIR ) CHIRON CORP.
PI Kavanaugh MW, Shyamala V;
DR WPI: 98-086965/08.
DR P-PSDB; W52169.
PT Human MKK3-interacting protein, used to identify human tissues in
PT malignant conditions - comprises nucleic acid, antibodies, fusion
PT proteins and peptide fragments
PS Disclosure; Page 14; 17pp; English.
CC This cDNA encodes a human MKK3-interacting protein (MIP). The mitogen-
CC activated protein kinase (WAPK) kinase-3 (MKK3) is a protein kinase that
CC phosphorylates p38 MAP kinase specifically and is involved in transducing
CC stress signals. The MIP binds to and interacts with a dominant
CC interfering mutant form of MKK3 and may be involved in transducing
CC extracellular signals to the nucleus, resulting in activation of p38
CC kinase. MIP is expressed in human brain, kidney, liver, lung, pancreas
CC and spleen but not in heart or striated muscle. Detection of MIP in a
CC body sample (particularly a tumour or metastasis) is used to identify the
CC tissue source, the tissue selected from the group consisting of brain,
CC kidney, liver, lung, pancreas or spleen tissue. Fusion proteins comprising
CC at least 8 contiguous amino acids of MIP fused to a second protein
CC sequence can be used to target MIP, or its peptides, to specific cells or
CC tissues. They can be used as a source of MIP in assays and also as
CC immunogen. The MIP encoding nucleic acid is used for expression of
CC recombinant MIP polypeptides and as a source of probes for detecting
CC MIP-related mRNA.
SQ Sequence 1698 BP; 455 A; 381 C; 449 G; 413 T;

Query Match 8.2%; Score 38; DB 40; Length 1698;
Best Local Similarity 95.1%; Pred. No. 5.35e-10;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 62 caggtaccggtccggaattcccggtgcaccacgcgctccg 102
QY 16 caggtancggtcagggaattcccggtgcaccacgcgctccg 56

RESULT 8
ID N81164 standard; DNA: 204 BP.
AC N81164;
DT 08-NOV-1990 (first entry)
DE Base substituted E.coli beta-galactosidase alpha-fragment.
KW E.coli beta galactosidase alpha-fragment; base substitutions; ss.
OS Escherichia coli.
FH Key Location/Qualifiers

```



CC affinity for a ligand and a second effector peptide portion that is  
 CC chemically or biologically active. They may further comprise a linker  
 CC peptide between the 2 domains. The oligonucleotides are also designed so  
 CC that the expressed peptide contains 2 or 4 cysteine residues positioned  
 CC in, or flanking, the unpredicted or variant residues. These residues  
 CC confer some degree of conformational rigidity to the peptides. The TSARs  
 CC or compans. comprising a TSAR binding domain can be used in vivo to  
 CC deliver a chemically or biologically active moiety, eg. metal ion,  
 CC radioisotope, peptide, toxin or enzyme, to the specific target or on the  
 CC cell. They can also replace the function of macromolecules, eg.  
 CC monoclonal or polyclonal antibodies and therefore circumvent the need  
 CC for complex methods of hybridoma formation or in vivo antibody  
 CC production. The TSARs are easily characterised and have designed  
 CC activity allowing direct and rapid detection in a screening process.  
 SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

Query Match 6.5%; Score 30; DB 12; Length 114;  
 Best Local Similarity 3.6%; Pred. No. 3.58e-05;  
 Matches 4; Conservative 31; Mismatches 77; Indels 0; Gaps 0;

Db 3 bnnbnnbnnbnnbgtcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnnnnn 62  
 QY 287 ggcaataatcgatccgcattccgcgctccatctcattcgttcgcaattcgttc 346  
 Db 63 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb 114  
 QY 347 tatctacgtcgtggaaggctgtggcaggacgcagagatcgttattctc 398

## RESULT 11

ID Q70467 standard; DNA; 114 BP.  
 AC Q70467;  
 DT 05-APR-1995 (first entry)  
 DE Generic DNA sequence to generate a random TSAR peptide library.  
 KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;  
 KW effector domain; concatenated heterofunctional protein; linker;  
 KW direct; rapid; detection; screening; treatment; generic; ss.  
 OS Synthetic.  
 FH Key  
 FT misc\_feature 55..60  
 FT /\*tag= a  
 FT /note= "this sequence represents '2'; 2 can be a  
 FT sequence of 6, 9 or 12 nucleotides (see  
 FT comments)"

WO9418318-A.  
 PD 18-AUG-1994.  
 PF 01-FEB-1994; U00977.  
 PR 01-FEB-1993; US-013416.  
 PR 30-DEC-1993; US-176500.  
 PR 31-JAN-1994; US-189331.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 PI Fowlkes DM, Kay BK;  
 DR WPI: 94-279739/34.  
 DR P-PSDB; R65153.  
 PT Identifying proteins or peptide(s) which bind a ligand - by  
 PT screening a recombinant vector library expressing fusion proteins  
 PT comprising a binding domain and an effector domain  
 PS Disclosure: Page 35: 255pp; English.  
 CC Q70467 is a generic DNA sequence used to generate random TSAR (Totally  
 CC Synthetic Affinity Reagents) peptides. This generic formula can also be  
 CC represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)1Y. X  
 CC and Y are flanking restriction sites (X is not the same as Y) that are  
 CC not specified further. Other generic sequences are shown in Q70466-68.  
 CC Other specific peptides generated by these generic sequences are shown in  
 CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,  
 CC comprising at least two functional regions - a binding domain with  
 CC affinity for a ligand and a second effector peptide portion that is  
 CC chemically or biologically active. They may further comprise a linker  
 CC peptide between the 2 domains. The oligonucleotides are also designed so  
 CC that the expressed peptide contains 2 or 4 cysteine residues positioned  
 CC in, or flanking, the unpredicted or variant residues. These residues  
 CC confer some degree of conformational rigidity to the peptides. The TSARs  
 CC or compans. comprising a TSAR binding domain can be used in vivo to

CC deliver a chemically or biologically active moiety, eg. metal ion,  
 CC radioisotope, peptide, toxin or enzyme, to the specific target or on the  
 CC cell. They can also replace the function of macromolecules, eg.  
 CC monoclonal or polyclonal antibodies and therefore circumvent the need for  
 CC complex methods of hybridoma formation or in vivo antibody production.  
 CC The TSARs are easily characterised and have designed activity allowing  
 CC direct and rapid detection in a screening process.  
 SQ Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;

Query Match 6.5%; Score 30; DB 12; Length 114;  
 Best Local Similarity 1.9%; Pred. No. 3.58e-05;  
 Matches 2; Conservative 31; Mismatches 73; Indels 0; Gaps 0;

Db 3 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnnnnnnn 62  
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 Db 63 bnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb 108  
 QY 365 gctgtggcaggacgcagagatcgcgtttattctcattcattcattcattcattc 410

## RESULT 12

ID Q70467 standard; DNA; 114 BP.  
 AC Q70467;  
 DT 05-APR-1995 (first entry)  
 DE Generic DNA sequence to generate a random TSAR peptide library.  
 KW TSAR; totally synthetic affinity reagent; synthetic; binding domain;  
 KW effector domain; concatenated heterofunctional protein; linker;  
 KW direct; rapid; detection; screening; treatment; generic; ss.  
 OS Synthetic.  
 FH Key  
 FT misc\_feature 55..60  
 FT /\*tag= a  
 FT /note= "this sequence represents '2'; 2 can be a  
 FT sequence of 6, 9 or 12 nucleotides (see  
 FT comments)"

WO9418318-A.  
 PD 18-AUG-1994.  
 PF 01-FEB-1994; U00977.  
 PR 01-FEB-1993; US-013416.  
 PR 30-DEC-1993; US-176500.  
 PR 31-JAN-1994; US-189331.  
 PA (UYNC-) UNIV NORTH CAROLINA.  
 PI Fowlkes DM, Kay BK;  
 DR WPI: 94-279739/34.  
 DR P-PSDB; R65153.  
 PT Identifying proteins or peptide(s) which bind a ligand - by  
 PT screening a recombinant vector library expressing fusion proteins  
 PT comprising a binding domain and an effector domain  
 PS Disclosure: Page 35: 255pp; English.  
 CC Q70467 is a generic DNA sequence used to generate random TSAR (Totally  
 CC Synthetic Affinity Reagents) peptides. This generic formula can also be  
 CC represented as follows: X(NNB)16(TGC)(NNB)12(NNB)16(TGC)(NNB)1Y. X  
 CC and Y are flanking restriction sites (X is not the same as Y) that are  
 CC not specified further. Other generic sequences are shown in Q70466-68.  
 CC Other specific peptides generated by these generic sequences are shown in  
 CC R65151-54. TSARs are concatenated heterofunctional proteins or peptides,  
 CC comprising at least two functional regions - a binding domain with  
 CC affinity for a ligand and a second effector peptide portion that is  
 CC chemically or biologically active. They may further comprise a linker  
 CC peptide between the 2 domains. The oligonucleotides are also designed so  
 CC that the expressed peptide contains 2 or 4 cysteine residues positioned  
 CC in, or flanking, the unpredicted or variant residues. These residues  
 CC confer some degree of conformational rigidity to the peptides. The TSARs  
 CC or compans. comprising a TSAR binding domain can be used in vivo to  
 CC deliver a chemically or biologically active moiety, eg. metal ion,  
 CC radioisotope, peptide, toxin or enzyme, to the specific target or on the  
 CC cell. They can also replace the function of macromolecules, eg.  
 CC monoclonal or polyclonal antibodies and therefore circumvent the need for  
 CC complex methods of hybridoma formation or in vivo antibody production.  
 CC The TSARs are easily characterised and have designed activity allowing  
 CC direct and rapid detection in a screening process.

[illegible]

Search completed: Mon Mar 8 22:14:25 1999  
Job time : 249 secs.

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Mar 8 22:40:59 1999; MasPar time 739.30 seconds  
Tabular output not generated. 1499.157 Million cell updates/sec

Title: >US-09-206-040-1  
Description: (1-469) from US09206040A.seq

Perfect Score: 465  
N.A. Sequence: 1 ttaacttcgacgncacagt.....gatgatactgaagatntt 469  
Comp: aattgaactcgcgcggtcca.....ctactatgtaacttctanna

Scoring table: TABLE jmetric

Gap 60

Nmatch STD : Dbase 0; Query 0

Searched: 602357 seqs, 1181590623 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: embl57

1:em\_ba 2:em\_fun 3:em\_htcg 4:em\_huml 5:em\_hum2 6:em\_in  
7:em\_om 8:em\_or 9:em\_ov 10:em\_pat 11:em\_ph 12:em\_pl  
13:em\_ro 14:em\_un 15:em\_v1

Database: genbank110

16:gb\_ba1 17:gb\_ba2 18:gb\_htg 19:gb\_in 20:gb\_om 21:gb\_ov  
22:gb\_pat 23:gb\_ph 24:gb\_pll 25:gb\_pi2 26:gb\_pl1  
27:gb\_pr2 28:gb\_pr3 29:gb\_ro 30:gb\_st 31:gb\_sts 32:gb\_sy  
33:gb\_un 34:gb\_v1

Statistics: Mean 8.428; Variance 2.694; scale 3.128

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	30	6.5	2125	28	AB016247 Homo sapiens mRNA for	6.08e-11
2	28	6.0	367	31	HSRSTS367 H. sapiens STS, 367bp,	5.65e-09
3	28	6.0	372	27	HSXS16 H. sapiens (xs16) mRNA,	5.65e-09
4	28	6.0	770	27	HSU77594 Human tazarotene-induc	5.65e-09
5	28	6.0	1009	24	AB010946 Arabidopsis thaliana m	5.65e-09
6	28	6.0	1214	29	AF019249 Mus musculus Nmi mRNA,	5.65e-09
7	28	6.0	1372	25	AF034255 Arabidopsis thaliana r	5.65e-09
8	28	6.0	1382	24	AF034255 Arabidopsis thaliana m	5.65e-09
9	28	6.0	1493	25	AF029216 Arabidopsis thaliana p	5.65e-09
10	28	6.0	1581	22	I60018 Sequence 1 from patent	5.65e-09
11	28	6.0	1640	24	AB000453 Petunia hybrida mRNA f	5.65e-09
12	28	6.0	1709	29	AF031814 Mus musculus pregnane	5.65e-09
13	28	6.0	1779	29	AF071316 Mus musculus COP9 comp	5.65e-09

14	28	6.0	2111	25	AF071862	Vigna unguiculata phos	5.65e-09
15	28	6.0	2351	25	AF060518	Cuphea pulcherrima 3-k	5.65e-09
16	28	6.0	2879	27	AF004231	Homo sapiens monocyte/	5.65e-09
17	28	6.0	3410	26	HSU27699	Human pepBCT-1 betain	5.65e-09
18	28	6.0	8665	28	HSU86136	Human telomerase-assoc	5.65e-09
19	27	5.8	1291	25	ATRNABIND	Arabidopsis thaliana m	5.21e-08
20	27	5.8	1500	21	XLNAKATP	X. laevis mRNA for Na,K	5.21e-08
21	27	5.8	1669	29	MMCARHOM	M. musculus mRNA for co	5.21e-08
22	27	5.8	2344	20	OCU36790	Oryctolagus cuniculus	5.21e-08
23	26	5.6	1829	24	ATU72153	Arabidopsis thaliana b	4.64e-07
24	22	4.7	1836	24	ATU39783	Arabidopsis thaliana a	1.97e-03
25	21	4.5	1257	22	I89416	Sequence 11 from patent	1.42e-02
26	21	4.5	1498	21	DRSAPK3	Danio rerio mRNA for s	1.42e-02
27	21	4.5	1627	20	PIGHRHR	Porcine growth hormone	1.42e-02
28	21	4.5	1712	24	ATAJ2414	Arabidopsis thaliana m	1.42e-02
29	21	4.5	2055	22	I89410	Sequence 3 from patent	1.42e-02
30	21	4.5	2345	29	AF090334	Mus musculus FK506 bin	1.42e-02
31	20	4.3	4701	29	AF022992	Mus musculus Rigu1 MRN	9.70e-02
32	20	4.3	5565	21	GGCOLVIA	Chicken COLVIA2 gene f	9.70e-02
33	20	4.3	41220	27	AC004777	Homo sapiens chromosom	9.70e-02
34	20	4.3	94482	25	ATF26P21	Arabidopsis thaliana D	9.70e-02
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37	19	4.1	1692	29	MMU87814	Mus musculus PEST phos	6.24e-01
38	19	4.1	1708	19	TRC223614	Tribolium castaneum mR	6.24e-01
39	19	4.1	2509	21	XLJ57455	Xenopus laevis growth	6.24e-01
40	19	4.1	3117	29	RNEWACA	R. norvegicus mRNA for	6.24e-01
41	19	4.1	4970	32	XXU13854	PGEX-4T2 cloning vecto	6.24e-01
42	19	4.1	4974	32	XXU13858	PGEX-5X3 cloning vecto	6.24e-01
43	19	4.1	4985	32	CVU78873	PGEX-6P-2 cloning vect	6.24e-01
44	19	4.1	33830	19	CEC04G2	Caenorhabditis elegans	6.24e-01
45	19	4.1	103566	27	AC003087	Human BAC clone Rg119H	6.24e-01

## ALIGNMENTS

RESULT	1	AB016247	2125 bp	mRNA	PRI	09-OCT-1998
LOCUS		Homo sapiens mRNA for sterol-C5-desaturase, complete cds.				
DEFINITION		AB016247				
ACCESSION		93721881				
NID		sterol-C5-desaturase; C5D.				
KEYWORDS		Homo sapiens (strain:caucasian) 9-year old female liver cDNA to mRNA.				
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						
MEDLINE						
REFERENCE						
AUTHORS						
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ACCESSION Y07966
NID g1552329
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SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 367)
AUTHORS McKie,A.B., Iwanura,T., Leung,H.Y., Hollingsworth,M.A. and
Lemoine,N.R.
TITLE Alu-polymerase chain reaction genomic fingerprinting technique
identifies multiple genetic loci associated with pancreatic
tumourigenesis
JOURNAL Genes Chromosomes Cancer 18 (1), 30-41 (1997)
MEDLINE 97147122
REFERENCE 2 (bases 1 to 367)
AUTHORS McKie,A.B.
TITLE Direct Submission
SUBMITTED (12-SEP-1996) A.B. McKie, ICRF Molecular Pathology Group,
8th Floor, MRC Cyclotron Bldg, Hammersmith Hosp, Duane Road,
London, W12 0NN, UK
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LOCUS
DEFINITION Human tazarotene-induced gene 2 (TIG2) mRNA, complete cds.
ACCESSION U77594
NID g1848263
KEYWORDS human.
SOURCE Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Homo.
REFERENCE 1 (bases 1 to 372)
AUTHORS Mueller-Pillasch,F., Gress,T., Lehrach,H. and Adler,G.
TITLE Differential gene expression in pancreatic cancer. Use of an
automated approach for the large scale isolation and
characterisation of cDNA clones containing differentially expressed
sequences
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 372)
AUTHORS Gress,T.
TITLE Direct Submission
SUBMITTED (16-AUG-1994) Gress T., University of Ulm, Department of
Internal Medicine I, Robert Koch Str.8, 89081 Ulm, Germany, 89081
REFERENCE 3 (bases 1 to 372)
AUTHORS Gress,T.M., Muller-Pillasch,F., Geng,M., Zimmerhackl,F.,
Zehetner,G., Friess,H., Buchler,M., Adler,G. and Lehrach,H.
TITLE A pancreatic cancer-specific expression profile
JOURNAL Oncogene 13 (8), 1819-1830 (1996)
MEDLINE 97050791
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Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3 GGAATCCCGGTCGACCCACGCGTCG 30
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RESULT 4 HSU77594 770 bp mRNA PRI 25-FEB-1997
LOCUS
DEFINITION Human tazarotene-induced gene 2 (TIG2) mRNA, complete cds.
ACCESSION U77594
NID g1848263
KEYWORDS human.
SOURCE Homo sapiens
Eukaryotae; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
AUTHORS Nagpat,S., Patel,S., Jacobs,H., Disepio,D., Ghosn,C., Malhotra,M.,
          Teng,M., Duvic,M. and Chandraratna,R.A.S.
TITLE    Tazarotene-induced gene 2 (TIG2), a novel retinoid responsive gene
          in skin
JOURNAL  Unpublished
REFERENCE 2 (bases 1 to 770)
AUTHORS  Nagpat,S., Patel,S. and Chandraratna,R.A.S.
TITLE    Direct Submission
JOURNAL  Submitted (06-NOV-1996) Biochemistry, Allergan Inc., 2525 Dupont
          Dr., Irvine, CA 92713, USA
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fibroblasts"
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PRS"
BASE COUNT 207 a 216 c 238 g 109 t
ORIGIN

Query Match 6.0%; Score 28; DB 27; Length 770;
Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 GGAATCCCGGTCGACCCACGCGTCG 36
|||||
QY 29 ggaattcccggtcgacccacgcgctcg 56

RESULT 5
LOCUS AB010946 1009 bp mRNA PLN 11-FEB-1998
DEFINITION Arabidopsis thaliana mRNA for Atrr1b, complete cds.
ACCESSION AB010946
NID 92865176
KEYWORDS Atrr1b.
SOURCE Arabidopsis thaliana (variety:columbia) cDNA to mRNA,
clone_lib:Lambda-PRL2 clone:143C4T7.
ORGANISM Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta;
Eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS Newman,T., de Bruijn,F.J., Green,P., Keegestra,K., Kende,H.,
          McIntosh,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M.,
          Retzel,E. and Somerville,C.
TITLE Gens galore: a summary of methods for accessing results from
          large-scale partial sequencing of anonymous Arabidopsis cDNA clones
          Plant Physiol. 106 (4), 1241-1255 (1994)
95148729
REFERENCE 2 (sites)
AUTHORS Sato,K., Ueda,T. and Nakano,A.
TITLE Identification of Arabidopsis thaliana RER1 homologues
          Unpublished (1998)
JOURNAL 3 (bases 1 to 1009)
REFERENCE Sato,K. and Nakano,A.
AUTHORS Direct Submission
TITLE Submitted (04-FEB-1998) to the DDBJ/EMBL/GenBank databases. Ken
          Sato, The Institute of Physical and Chemical Research(RIKEN),
          Molecular Membrane Biology Laboratory; 2-1 Hirosawa, Wako, Saitama
          351-0106, Japan [E-mail:satoken@postman.riken.go.jp,
          Tel:+81-48-467-9548, Fax:+81-48-462-4679)

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152..739
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152..739
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EFKPIRLPEKFWYSMTKAFCLAFMTFESVDFVPVFWPILLICYWVLFVLTMRRO
IAHMIKHKIIPFSIGKQKYSKGRSSANGSGSRAD"
BASE COUNT 253 a 226 c 212 g 318 t
ORIGIN

Query Match 6.0%; Score 28; DB 24; Length 1009;
Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GGAATCCCGGTCGACCCACGCGTCG 28
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QY 29 ggaattcccggtcgacccacgcgctcg 56

RESULT 6
LOCUS AF019249 1214 bp mRNA ROD 22-SEP-1997
DEFINITION Mus musculus Nmi mRNA, complete cds.
ACCESSION AF019249
NID 92425059
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
          Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Mehtani,S. and Zervos,A.S.
TITLE Mouse homologue of the human Nmi cDNA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1214)
AUTHORS Mehtani,S. and Zervos,A.S.
TITLE Direct Submission
JOURNAL Submitted (13-AUG-1997) Cutaneous Biology Research Center,
          Massachusetts General Hospital, Harvard Medical School, 13th
          Street, Bldg. 149, Charlestown, MA 02129, USA
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source   Location/Qualifiers
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150..1094
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KKTYPLYNQKCHSVAPCIERLEKYQVFSVSKKTVLLTGLTLEGIPVDEETGEDI
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BASE COUNT 395 a 244 c 314 g 261 t
ORIGIN

Query Match 6.0%; Score 28; DB 29; Length 1214;
Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 GGAATTCCTGGGTGACCCACGCGTCCG 30
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Qy 29 ggaattccgggtgacccacgcgtccg 56

RESULT 7
LOCUS AFO34255 1372 bp mRNA PLN 01-MAY-1998
DEFINITION Arabidopsis thaliana reversibly glycosylated polypeptide-3 (RGP)
ACCESSION AF034255
NID 92645970
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 1372)
AUTHORS Delgado, I. J., Wang, Z., de Rocher, A., Keegstra, K. and Raikhel, N. V.
TITLE Cloning and characterization of AtRGP1. A reversibly
autoglycosylated arabidopsis protein implicated in cell wall
biosynthesis
JOURNAL Plant Physiol. 116 (4), 1339-1350 (1998)
MEDLINE 98205072
REFERENCE 2 (bases 1 to 1372)
AUTHORS Delgado, I., Wang, Z., de Rocher, A., Keegstra, K. and Raikhel, N. V.
TITLE Direct Submission
JOURNAL Submitted (13-NOV-1997) Genetics, MSU-DOE-Plant Research
Laboratory, 122 Plant Biology Building, East Lansing, MI
48824-1312, USA
FEATURES
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/db_xref="taxon:3702"
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PFLUREGVSTAVSHGLWLPDADPTQLYPKERNTRYDVAWMTIPKGLFFMCGMN
LAFDELIGPAMVFLMGDGPIDGRYDDMWAGCIVICDHLGLGVTGLPYTHSKA
SNPFVNLKVKYGIWFQEEIIPFONAKLSKEAVTVQOCYIELSKMVKELSLDPYF
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BASE COUNT 364 a 315 c 307 g 386 t
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Query Match 6.0%; Score 28; DB 25; Length 1372;
Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 GGAATTCCTGGGTGACCCACGCGTCCG 39
      |||||||
Qy 29 ggaattccgggtgacccacgcgtccg 56

RESULT 8
LOCUS ATRSP40 1382 bp RNA PLN 31-OCT-1997
DEFINITION Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor,
RSP40.
ACCESSION X99437
NID 92582640
KEYWORDS splicing factor.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 1382)
AUTHORS Kranz, H. D., Denekamp, M., Grisco, R., Jin, H.-L., Leyva, A.,
Meissner, R., Petroni, K., Urzainqui, A., Bevan, M., Martin, C.,
Smeekens, S., Tonelli, C., Paz-Ares, J. and Weisshaar, B.
TITLE Towards functional characterisation of the members of the R2R3-MYB

Embryophyta; vascular plants; seed plants; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1382)
AUTHORS Lopato, S., Waigmann, E. and Barta, A.
TITLE Characterization of a novel arginine/serine-rich splicing factor in
Arabidopsis
Plant Cell 8 (12), 2255-2264 (1996)
97143875
REFERENCE 2 (bases 1 to 1382)
AUTHORS Barta, A.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-1996) A. Barta, Institut of Biochemistry,
University of Vienna, Vienna Biocenter, Dr. Bohrgasse 9/3, A-1030
Vienna, AUSTRIA
REMARK 3 (bases 1 to 1382)
AUTHORS Barta, A.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1997) A. Barta, Institut of Biochemistry,
University of Vienna, Vienna Biocenter, Dr. Bohrgasse 9/3, A-1030
Vienna, AUSTRIA
COMMENT On Nov 2, 1997 this sequence version replaced gi:1707367.
Related sequence: T20696.
FEATURES
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146. .1198
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ISVEYAVKDDARGHSPERRRDRSPRRRSPSPYKRRGSPDYGRGASPVAAAKA
ERTSPDYGRRRSPYKRRGSPYGRDRGRNDSPRRRERVASPTKYGRSPNNKPKA
MSPNHSFPKKSPPRGVGEVSPERRRERSRSPENGQVSPSGIGRRSDGQYEWAC
SPMQKSRSPRPPADE"
BASE COUNT 406 a 274 c 390 g 312 t
ORIGIN
Query Match 6.0%; Score 28; DB 24; Length 1382;
Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 GGAATTCCTGGGTGACCCACGCGTCCG 81
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Qy 29 ggaattccgggtgacccacgcgtccg 56

RESULT 9
LOCUS AF062916 1493 bp mRNA PLN 02-DEC-1998
DEFINITION Arabidopsis thaliana putative transcription factor (MYB92) mRNA,
complete cds.
ACCESSION AF062916
NID 93941523
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 1493)
AUTHORS Kranz, H. D., Denekamp, M., Grisco, R., Jin, H.-L., Leyva, A.,
Meissner, R., Petroni, K., Urzainqui, A., Bevan, M., Martin, C.,
Smeekens, S., Tonelli, C., Paz-Ares, J. and Weisshaar, B.
TITLE Towards functional characterisation of the members of the R2R3-MYB

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JOURNAL MEDLINE  
 REFERENCE 99056848  
 AUTHORS Melssner,R., Jin,H.-L., Martin,C. and Bevan,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-MAY-1998) Abt. Biochemie, MPI fur Zuchtungsforschung, Carl-von-Linne-Weg 10, Koeln D-50829, Germany

## FEATURES

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BASE COUNT 470 a 321 c 290 g 412 t  
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Query Match 6.0%; Score 28; DB 25; Length 1493;  
 Best Local Similarity 100.0%; Pred. No. 5,65e-09;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 25 GGAATTCGCGGTGACCCACGCGTCGC 52  
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 QY 29 ggaattccgggtgacccacgcgcgcg 56

RESULT 10  
 LOCUS I60018 1581 bp DNA PAT 15-AUG-1997  
 DEFINITION Sequence 1 from patent US 5654495.  
 ACCESSION I60018  
 NID 92478650

KEYWORDS Unknown.  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 1581)  
 AUTHORS Voelker,F.Alois and Davies,H.Maelor.  
 TITLE Production of myristate in plant cells  
 JOURNAL Patent: US 5654495-A 1 05-AUG-1997;  
 FEATURES Location/Qualifiers  
 source  
 1. .1581  
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 BASE COUNT 418 a 336 c 410 g 397 t  
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 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 54 GGAATTCGCGGTGACCCACGCGTCGC 81  
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 QY 29 ggaattccgggtgacccacgcgcgcg 56

RESULT 11  
 LOCUS AB000453 1640 bp mRNA PLN 28-JAN-1997

DEFINITION  
 ACCESSION AB000453  
 NID g1786137  
 KEYWORDS  
 SOURCE

## ORGANISM

Petunia hybrida mRNA for PETHy:ZPT3-1, complete cds.  
 Petunia hybrida (cultivar:Mitchell diploid, lab\_host:Escherichia coli, DH10B) stamen cDNA to mRNA, clone:ZPT3-1.  
 Petunia x hybrida  
 Eukaryotae; mitochondrial eukaryotes; Viridiplantae;  
 Charophyta/Embryophyta group; Embryophyta; vascular plants; seed  
 plants; Magnoliophyta; Magnoliopsida; Solanaceae; Solanales;  
 Solanaceae; Petunia.  
 1 (sites)  
 Kobayashi,A., Sakamoto,A., Kubo,K., Rybka,Z., Kanno,Y. and  
 Takatsuji,H.  
 TITLE Seven zinc-finger transcription factors are expressed sequentially during the development of anthers and pollen in Petunia  
 JOURNAL Unpublished (1997)  
 REFERENCE 2 (bases 1 to 1640)  
 AUTHORS Takatsuji,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-JAN-1997) to the DDBJ/EMBL/GenBank databases. Hiroshi Takatsuji, National Institute of Agrobiological Resources, Plant Physiology, 2-1-2 Kannondai, Tsukuba, Ibaraki 305, Japan (tel:0298-38-8383, fax:0298-38-7417)

## FEATURES

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BASE COUNT 579 a 300 c 327 g 434 t  
 ORIGIN

Query Match 6.0%; Score 28; DB 24; Length 1640;  
 Best Local Similarity 100.0%; Pred. No. 5,65e-09;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 GGAATTCGCGGTGACCCACGCGTCGC 36  
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 QY 29 ggaattccgggtgacccacgcgcgcg 56

## RESULT 12

LOCUS AF031814 1709 bp mRNA ROD 08-FEB-1998  
 DEFINITION Mus musculus pregnane x receptor mRNA, complete cds.  
 ACCESSION AF031814  
 NID 92852328

KEYWORDS house mouse.  
 SOURCE Mus musculus

## ORGANISM

Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;  
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 1709)  
 Klierer,S.A., Moore,J.T., Wade,L., Staudinger,J.L., Watson,M.A.,  
 Jones,S.A., McKee,D.D., Oliver,B.B., Willson,T.M.,  
 Zetterstrom,R.H., Perlmann,T. and Lehmann,J.M.

## TITLE

An orphan nuclear receptor activated by pregnanes defines a novel

```

steroid signaling pathway
Cell 92 (1), 73-82 (1998)
98149345
REFERENCE
AUTHORS
Kliwer, S.A., Moore, J.T., Wade, L., Staudinger, J.L., Watson, M.A.,
Jones, S.A., McKee, D.D., Oliver, B.B., Willson, T.M.,
Zetterstrom, R.H., Perlmann, T. and Lehmann, J.M.
TITLE
Direct Submission
JOURNAL
Submitted (29-0CT-1997) Department of Molecular Endocrinology,
Glaxo Wellcome, 5 Moore Drive, RTP, NC 27709, USA
FEATURES
Location/Qualifiers
1. .1709
/organism="Mus musculus"
/db_xref="taxon:10090"
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IWNQPKPSDQKTEIPLPLHADVSTYMFKNFAKVISYFRDLPTIEDQISLKG
TEYICILFRNTFMOTCTWECGLAYCFDPNGFGFKLLDPLMKFCHMLKQLQKH
EYVILMOAISLSPDRPGVQVRSVVDQLOERFALTAKYIECSRYPFAHRELFKLKMA
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BASE COUNT 449 a 444 c 468 g 348 t
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Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 GGAATTCGGGTGACCCACGCGTCCG 35
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Qy 29 ggaattccgggtgacccacgctccg 56

RESULT 13
LOCUS AF071316 1779 bp mRNA 03-SEP-1998
DEFINITION Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.
ACCESSION AF071316
NID 93309173
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Wei, N., Tsuge, T., Serino, G., Dohmae, N., Takio, K., Matsui, M. and
Deng, X.-W.
TITLE The COP9 complex is conserved between plants and mammals and is
related to the 26S proteasome regulatory complex
JOURNAL Curr. Biol. 8 (16), 919-922 (1998)
MEDLINE 98372877
REFERENCE
AUTHORS Wei, N., Tsuge, T., Dohmae, N., Takio, K., Matsui, M. and Deng, X.-W.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1998) Department of Molecular, Cellular, and
Developmental Biology, Yale University, 165 Prospect Street, New
Haven, CT 06511, USA
FEATURES Location/Qualifiers
1. .1779
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1. .1779
/gene="COP87a"
159. .986
/gene="COP87a"

steroid signaling pathway
Cell 92 (1), 73-82 (1998)
98149345
REFERENCE
AUTHORS
Kliwer, S.A., Moore, J.T., Wade, L., Staudinger, J.L., Watson, M.A.,
Jones, S.A., McKee, D.D., Oliver, B.B., Willson, T.M.,
Zetterstrom, R.H., Perlmann, T. and Lehmann, J.M.
TITLE
Direct Submission
JOURNAL
Submitted (29-0CT-1997) Department of Molecular Endocrinology,
Glaxo Wellcome, 5 Moore Drive, RTP, NC 27709, USA
FEATURES
Location/Qualifiers
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IWNQPKPSDQKTEIPLPLHADVSTYMFKNFAKVISYFRDLPTIEDQISLKG
TEYICILFRNTFMOTCTWECGLAYCFDPNGFGFKLLDPLMKFCHMLKQLQKH
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BASE COUNT 449 a 444 c 468 g 348 t
ORIGIN

Query Match 6.0%; Score 28; DB 29; Length 1709;
Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 GGAATTCGGGTGACCCACGCGTCCG 35
|||||
Qy 29 ggaattccgggtgacccacgctccg 56

RESULT 13
LOCUS AF071316 1779 bp mRNA 03-SEP-1998
DEFINITION Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds.
ACCESSION AF071316
NID 93309173
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS Wei, N., Tsuge, T., Serino, G., Dohmae, N., Takio, K., Matsui, M. and
Deng, X.-W.
TITLE The COP9 complex is conserved between plants and mammals and is
related to the 26S proteasome regulatory complex
JOURNAL Curr. Biol. 8 (16), 919-922 (1998)
MEDLINE 98372877
REFERENCE
AUTHORS Wei, N., Tsuge, T., Dohmae, N., Takio, K., Matsui, M. and Deng, X.-W.
TITLE Direct Submission
JOURNAL Submitted (11-JUN-1998) Department of Molecular, Cellular, and
Developmental Biology, Yale University, 165 Prospect Street, New
Haven, CT 06511, USA
FEATURES Location/Qualifiers
1. .1779
/organism="Mus musculus"
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BASE COUNT 449 a 444 c 468 g 348 t
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Query Match 6.0%; Score 28; DB 29; Length 1779;
Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 GGAATTCGGGTGACCCACGCGTCCG 33
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Qy 29 ggaattccgggtgacccacgctccg 56

RESULT 14
LOCUS AF071862 2111 bp mRNA 23-JUN-1998
DEFINITION Vigna unguiculata phosphoribosylpyrophosphate amidotransferase
(pur1) mRNA, complete cds.
ACCESSION AF071862
NID 93243255
KEYWORDS cowpea.
SOURCE Vigna unguiculata
ORGANISM Eukaryota; Viridiplantae; Charophyta; Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta;
eudicotyledons; Rosidae; Fabales; Fabaceae; Papilionoideae; Vigna.
REFERENCE
AUTHORS Mann, A.J., Smith, P.M.C. and Atkins, C.A.
TITLE Vigna unguiculata phosphoribosylpyrophosphate amidotransferase
2 (bases 1 to 2111)
JOURNAL Unpublished
REFERENCE
AUTHORS Mann, A.J., Smith, P.M.C. and Atkins, C.A.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1998) Botany, University of Western Australia,
Perth, WA 6907, Australia
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 5.65e-09;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 6 GGAATTCGGGTGACCCACGCGTCCG 33
|||||
Qy 29 ggaattccgggtgacccacgctccg 56

RESULT 14
LOCUS AF071862 2111 bp mRNA 23-JUN-1998
DEFINITION Vigna unguiculata phosphoribosylpyrophosphate amidotransferase
(pur1) mRNA, complete cds.
ACCESSION AF071862
NID 93243255
KEYWORDS cowpea.
SOURCE Vigna unguiculata
ORGANISM Eukaryota; Viridiplantae; Charophyta; Embryophyta group;
Embryophyta; Tracheophyta; seed plants; Magnoliophyta;
eudicotyledons; Rosidae; Fabales; Fabaceae; Papilionoideae; Vigna.
REFERENCE
AUTHORS Mann, A.J., Smith, P.M.C. and Atkins, C.A.
TITLE Vigna unguiculata phosphoribosylpyrophosphate amidotransferase
2 (bases 1 to 2111)
JOURNAL Unpublished
REFERENCE
AUTHORS Mann, A.J., Smith, P.M.C. and Atkins, C.A.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-1998) Botany, University of Western Australia,
Perth, WA 6907, Australia
FEATURES Location/Qualifiers
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/gene="pur1"
45. .1748
/EC_number="2.4.2.14"
/feature="PRAT"
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BASE COUNT 497 a 568 c 532 g 514 t  
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Best Local Similarity 100.0%; Pred. No. 5.65e-09;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 8 GGAATTCGGGTCGACCGCGTCGC 35

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Qy 29 ggaattccgggtcgaccacgcgctcg 56

RESULT 15

LOCUS AF060518 2351 bp mRNA PLN 28-OCT-1998  
DEFINITION Cuphea pulcherrima 3-ketoacyl-ACP synthase (Kas4) mRNA, complete cds.

ACCESSION AF060518

NID g3800746

KEYWORDS Cuphea pulcherrima.

SOURCE Cuphea pulcherrima

ORGANISM

Eukaryota; Viridiplantae; Charophyta/Embryophyta group;  
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;  
Magnoliophyta; eudicotyledons; Rosidae; Myrtales; Lythraceae;  
Cuphea.

REFERENCE 1 (bases 1 to 2351)

AUTHORS Dehesh, K., Edwards, P., Fillatti, J., Slabaugh, M. and Byrne, J.

TITLE KAS IV: a 3-ketoacyl-ACP synthase from Cuphea sp. is a medium chain

specific condensing enzyme

JOURNAL Plant J. 15 (3), 383-390 (1998)

MEDLINE 98422743

REFERENCE 2 (bases 1 to 2351)

AUTHORS Dehesh, K.

TITLE Direct Submission

JOURNAL Submitted (20-APR-1998) Oils division, Calgene, 1920 Fifth Street,

Davis, CA 9561, USA

FEATURES Location/Qualifiers

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GFVACRALSORNSDPTKAGRPMDNSRDFVMGEGAGVLLLELEHAHKKRGATIIAEFL  
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BASE COUNT 613 a 563 c 537 g 537 t 1 others

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.65e-09;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 23 GGAATTCGGGTCGACCGCGTCGC 50

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Qy 29 ggaattccgggtcgaccacgcgctcg 56

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QY 330 ttgccacttctgcttatctatctagctgctg 360

RESULT 2
LOCUS HSRSTS367 367 bp RNA STS 16-SEP-1997
DEFINITION H.sapiens STS, 367bp, sequence tagged site.
ACCESSION Y07966
NID 9152329
KEYWORDS STS; sequence tagged site.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 367)
AUTHORS McKie,A.B., Iwamura,T., Leung,H.Y., Hollingsworth,M.A. and
Lemoine,N.R.
TITLE Alu-polymerase chain reaction genomic fingerprinting technique
identifies multiple genetic loci associated with pancreatic
tumorigenesis
JOURNAL Genes Chromosomes Cancer 18 (1), 30-41 (1997)
MEDLINE 97147122
REFERENCE 2 (bases 1 to 367)
AUTHORS McKie,A.B.
TITLE Direct Submission
JOURNAL Submitted (12-SEP-1996) A.B. McKie, ICRF Molecular Pathology Group,
8th Floor, MRC Cyclotron Bldg, Hammersmith Hosp, Ducane Road,
London, W12 0NN, UK
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Best Local Similarity 95.1%; Pred.No. 2.19e-09;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 29 CAGGTACCGGTCCGGATTCGCCGGTCGACCCACGCGTCCG 69
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QY 16 caggtancggtcaggaattccgggtcgaccacgcgctccg 56

RESULT 3
LOCUS ATRSP40 1382 bp RNA PLN 31-OCT-1997
DEFINITION Arabidopsis thaliana mRNA for arginine/serine-rich splicing factor,
RSP40
ACCESSION X99437
NID 92582640
KEYWORDS splicing factor..
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryotae; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; vascular plants; seed plants; Magnoliophyta;
Magnoliopsida; Capparales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1382)
AUTHORS Lopato,S., Waigmann,E. and Barta,A.
TITLE Characterization of a novel arginine/serine-rich splicing factor in
Arabidopsis
JOURNAL Plant Cell 8 (12), 2255-2264 (1996)
MEDLINE 97143875
REFERENCE 2 (bases 1 to 1382)
AUTHORS Barta,A.
TITLE Direct Submission
JOURNAL Submitted (18-JUL-1996) A. Barta, Institut of Biochemistry,
University of Vienna, Vienna Biocenter, Dr. Bohrgasse 9/3, A-1030
Vienna, AUSTRIA

QY 330 ttgccacttctgcttatctatctagctgctg 360

Revised by [3]
REFERENCE 3 (bases 1 to 1382)
AUTHORS Barta,A.
TITLE Direct Submission
JOURNAL Submitted (30-OCT-1997) A. Barta, Institut of Biochemistry,
University of Vienna, Vienna Biocenter, Dr. Bohrgasse 9/3, A-1030
Vienna, AUSTRIA
COMMENT On Nov 2, 1997 this sequence version replaced gi:1707367.
Related sequence: T20696.
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Location/Qualifiers
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ISVEYAKDDDARGHSPERRRSPSPYKRRERGSPTDGRGASPLVATYK
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BASE COUNT 406 a 274 c 390 g 312 t
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Best Local Similarity 95.1%; Pred.No. 2.19e-09;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 41 CAGGTACCGGTCCGGATTCGCCGGTCGACCCACGCGTCCG 81
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QY 16 caggtancggtcaggaattccgggtcgaccacgcgctccg 56

RESULT 4
LOCUS AF062916 1493 bp mRNA PLN 02-DEC-1998
DEFINITION Arabidopsis thaliana putative transcription factor (MYB92) mRNA,
complete cds.
ACCESSION AF062916
NID 93941523
KEYWORDS thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae;
Arabidopsis.
REFERENCE 1 (bases 1 to 1493)
AUTHORS Kranz,H.D., Denekamp,M., Greco,R., Jin,H.-L., Leyva,A.,
Meissner,R., Petroni,K., Urzainqui,A., Bevan,M., Martin,C.,
Smeekens,S., Tonelli,C., Paz-Ares,J. and Weisshaar,B.
TITLE Towards functional characterisation of the members of the R2R3-MYB
gene family from Arabidopsis thaliana
JOURNAL Plant J. 16 (2), 263-276 (1998)
MEDLINE 99056848
REFERENCE 2 (bases 1 to 1493)
AUTHORS Meissner,R., Jin,H.-L., Martin,C. and Bevan,M.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-1998) Abt. Biochemie, MPI fur Zuchtungsforshung,
Carl-von-Linne-Weg 10, Koeln D-50929, Germany
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ORIGIN

Query Match      8.2%; Score 38; DB 25; Length 1493;
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Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 16 caggtancggtcaggattcccggtgcacccacgcgctccg 56

RESULT 5
LOCUS 160018 1581 bp DNA PAT 15-AUG-1997
DEFINITION Sequence 1 from patent US 5654495.
ACCESSION 160018
NID 92478650
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1581)
AUTHORS Voelker,T.Alois and Davies,H.Maelor.
TITLE Production of myristate in plant cells
JOURNAL Patent: US 5654495-A 1 05-AUG-1997;
FEATURES Location/Qualifiers
source
1. .1581
BASE COUNT 418 a 356 c 410 g 397 t
ORIGIN

Query Match      8.2%; Score 38; DB 22; Length 1581;
Best Local Similarity 95.1%; Pred. No. 2.19e-09;
Matches 39; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 41 CAGGTACCGGTCCGGAAATTCCTGGGTGCACCCAGCGCTCCG 81
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QY 16 caggtancggtcaggattcccggtgcacccacgcgctccg 56

RESULT 6
LOCUS AF060518 2351 bp mRNA PLN 28-OCT-1998
DEFINITION Cuphea pulcherrima 3'-ketoacyl-ACP synthase (Kas4) mRNA, complete cds.
ACCESSION AF060518
NID 93800746
KEYWORDS
SOURCE Cuphea pulcherrima.
ORGANISM Cuphea pulcherrima
Eukaryota; Viridiplantae; Charophyta/Embryophyta group;
Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; Myrtales; Lythraceae;
Cuphea.
REFERENCE 1 (bases 1 to 2351)
AUTHORS Dehesh,K., Edwards,P., Fillatti,J., Siabaugh,M. and Byrne,J.
TITLE KAS IV: a 3'-ketoacyl-ACP synthase from Cuphea sp. is a medium chain

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[illegible]

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RESULT 8
LOCUS AF012089 10772 bp DNA INV 05-AUG-1997
DEFINITION Drosophila melanogaster cysteine proteinase-1 (Cp1) gene, complete
cds, and phenylalanyl tRNA synthetase gene, partial cds.
ACCESSION AF012089
NID g2305220
KEYWORDS
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Eukaryota; mitochondrial eukaryotes; Metazoa; Arthropoda;
Tracheata; Hexapoda; Insecta; Pterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 4546 to 4553)
AUTHORS Gray, Y.H.M., Tanaka, M.M. and Sved, J.A.
TITLE P-element-induced recombination in Drosophila melanogaster: hybrid
element insertion
JOURNAL Genetics 144 (4), 1601-1610 (1996)
MEDLINE 97132596
REFERENCE 2 (bases 1 to 10772)
AUTHORS Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
TITLE Structure of the cysteine proteinase (Cp1) gene of Drosophila
melanogaster and associated mutational effects
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 10772)
AUTHORS Gray, Y.H.M., Sved, J.A., Preston, C.R. and Engels, W.R.
TITLE Direct Submission
JOURNAL Submitted (30-JUN-1997) School of Biological Sciences, University
of Sydney, Biology A12, Sydney University, NSW 2006, Australia
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/translation="MRTAVLLPLALLAAVAQVAFADVVMEWTFKLEHKKVQDET
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6751..7707
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6691..6750
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6751..7707
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1001..2309
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HFRSGVLSQNLVDSTKYGNGCNGGLMDNAPRIKONGGIDIKERSYPYEAID
DFSKNGVTGADRDFTDIPQDGEKMAEAVATGPVPSVDAIDASHESQFYSEGVYN
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BASE COUNT 2929 a 2357 c 2282 g 3046 t 158 others
ORIGIN

Query Match 8.0%; Score 37; DB 19; Length 10772;
Best Local Similarity 20.6%; Pred. No. 1.05e-08;
Matches 22; Conservative 55; Mismatches 28; Indels 2; Gaps 2;

Db 1691 AKRWYAWNTTMMKMWTKMKWMTYRTWMMKMYW-TSRTTTTSAMMMWYTWSTWT 1749
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Cp 250 attttgaaatcaatgcaaatcttatgcaacgatgatgatgatgatgatg-at 192
::: | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
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|: ::: | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Cp 191 gcagagagaattggaatgacatgcagatgacagaaagcaagtcctt 145
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RESULT 10
LOCUS AC005369 74371 bp DNA PRI 01-AUG-1998
DEFINITION Homo sapiens chromosome 5, BAC clone 119j3 (LBNL H175), complete
sequence.
ACCESSION AC005369
NID g3367505
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1 (bases 1 to 74371)
AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miguel,T., Miller,C., Pittluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE Sequencing of human chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 74371)
AUTHORS Ricke,D.O.
TITLE Large Scale Sequence Analysis and Annotation with the Sequence
Comparison Analysis (SCAN) System
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 74371)
AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Davis,C.A., Kadner,K., Miguel,T., Pittluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
COMMENT Sequence submitted by:
DOE Joint Genome Institute.
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5327. .5602
/rpt_family="Alu"
6586. .6956
/rpt_family="L1"
6847. .6884
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complement(7830. .8185)
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9070. .9387
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complement(9740. .9845)
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complement(10440. .11015)
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Best Local Similarity 94.9%; Pred. No. 5.00e-08;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 GGTACCGTCCGGATTCCCGGGTCGACCCACCGGTCG 39
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Qy 18 ggtancggtcaggattcccggtcgacccacggtccg 56
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RESULT 14
LOCUS HSU77594 770 bp mRNA PRI 25-FEB-1997
DEFINITION Human tazarotene-induced gene 2 (TIG2) mRNA, complete cds.
ACCESSION U77594
NID 91848263
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 770)
AUTHORS Nagpat,S., Patel,S., Jacobs,H., DiSepio,D., Ghosh,C., Malhotra,M.,
Teng,M., Duvic,M. and Chandraratna,R.A.S.
Tazarotene-induced gene 2 (TIG2), a novel retinoid responsive gene
in skin
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 770)
AUTHORS Nagpal,S., Patel,S. and Chandraratna,R.A.S.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-1996) Biochemistry, Allergan Inc., 2525 Dupont
Dr., Irvine, CA 92713, USA
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Best Local Similarity 94.9%; Pred. No. 5.00e-08;
Matches 37; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 GGTACCGTCCGGATTCCCGGGTCGACCCACCGGTCG 39
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RESULT 15
LOCUS AB000453 1640 bp mRNA PLN 28-JAN-1997
DEFINITION Petunia hybrida mRNA for PETHY.ZPT3-1, complete cds.
ACCESSION AB000453
NID 91786137
KEYWORDS zinc finger protein; ZPT3; transcription factor.
SOURCE Petunia hybrida (cultivar:Mitchell diploid, lab_host:Escherichia
coli, DH10B) stamen cDNA to mRNA, clone:ZPT3-1.
ORGANISM Petunia x hybrida
Eukaryota; mitochondrial eukaryotes; Viridiplantae;
Charophyta/Embryophyta group; Embryophyta; vascular plants; seed
plants; Magnoliophyta; Magnoliopsida; Solananae; Solanales;
Solanaceae; Petunia.
REFERENCE 1 (sites)
AUTHORS Kobayashi,A., Sakamoto,A., Kubo,K., Rybka,Z., Kanno,Y. and
Takatsuji,H.
TITLE Seven zinc-finger transcription factors are expressed sequentially
during the development of anthers and pollen in Petunia
JOURNAL Unpublished (1997)
REFERENCE 2 (bases 1 to 1640)
AUTHORS Takatsuji,H.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1997) to the DDBJ/EMBL/GenBank databases. Hiroshi
Takatsuji, National Institute of Agrobiological Resources, Plant
Physiology, 2-1-2 Kannondai, Tsukuba, Ibaraki 305, Japan
(Tel:0298-38-8383, Fax:0298-38-7417)
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Query Match 7.1%; Score 33; DB 24; Length 1640;
Best Local Similarity 94.4%; Pred. No. 4.85e-06;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 ACCGGTCCGGAATTCGCGGTGACCCACCGGTCG 36
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Qy 21 ancggtcaggattcccggtcgacccacggtccg 56
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